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		MAUE		
	APPLICATION NUMBER	FILING/RECEIPT DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO /TITLE
-				

12/31/97

MIZZEN

870109.408

SEED AND BERRY 6300 COLUMBIA CENTER 701 FIFTH AVENUE SEATTLE WA 99104-7092

DATE MAILED:

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS

CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLO	SURES
The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):	the
1. This application fails to comply with the requirements of 37 CFR 1.821 - 1.825.	· .
This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence required by 37 CFR 1.821(c).	Listing" as
A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).	<i>I</i>
4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the co-computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.832, as attached marked-up copy of the "Raw Sequence Listing."	
5. The computer readable form that has been filed with this application has been found to be damage unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable submitted as required by 37 CFR 1.825(d).	
6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "S Listing" as required by 37 CFR 1.821(e).	equence
APPLICANT MUST PROVIDE: An initial or substitute computer readable form (CRF) copy of the "Sequence Listing." An initial or substitute paper copy of the "Sequence Listing," as well as an amendment directing its specification. A statement that the content of the paper and computer readable copies are the same and, where include no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b) or 1.825(d).	
FOR QUESTIONS REGARDING COMPLIANCE WITH THESE REQUIREMENTS, PLEASE CONTACT: For Rules Interpretation, call (703) 308-1123. For CRF submission help, call (703) 308-4212. For Patentin software help, call (703) 308-6856.	
	1

Form PTO-1661 (Rev. 7-96)

Customer Service Center

Initial/Patent Examination Division (703) 308-1202



SEOUENCE LISTING

- (1) GENERAL INFORMATION:
 - (i) APPLICANTS: Mizzen, Lee Wisniewski, Jan
 - (ii) TITLE OF INVENTION: STREPTOCACCAL HEAT SHOCK PROTEINS OF THE HSP60 FAMILY
 - (iii) NUMBER OF SEQUENCES: 91
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: SEED and BERRY LLP
 - (B) STREET: 701 Fifth Avenue, 6300 Columbia Center
 - (C) CITY: Seattle
 - (D) STATE: Washington
 - (E) COUNTRY: USA
 - (F) ZIP: 98104
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/001,737
 - (B) FILING DATE: 31-DEC-1997
 - (C) CLASSIFICATION:
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Sharkey, Richard G.
 - (B) REGISTRATION NUMBER: 32,629
 - (C) REFERENCE/DOCKET NUMBER: 870109.408
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (206) 622-4900
 - (B) TELEFAX: (206) 682-6031
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1665 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 15..1649
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCGGCT TCAT			A AAA TTC GGT AAC GA L Lys Phe Gly Asn As 10	
			A CTG GCA GAT GCA GT L Leu Ala Asp Ala Va 25	
	Pro Lys Gl		A GTT CTG GAT AAA TC L Val Leu Asp Lys Se 40	
			T TCC GTA GCA CGT GA L Ser Val Ala Arg Gl 55	
			r GCG CAG ATG GTG AA / Ala Gln Met Val Ly) 7	
			GAC GGT ACC ACC AC Asp Gly Thr Thr Th 90	
			A GGC CTG AAA GCC GT 1 Gly Leu Lys Ala Va 105	
		p Leu Lys Arg	GGT ATC GAC AAA GG GGT Ile Asp Lys Al 120	
			G TCC GTA CCG TGC TC 1 Ser Val Pro Cys Se 135	
			C TCC GCT AAC TCC GA e Ser Ala Asn Ser As) 15	p Glu
			G GAC AAA GTC GGT AA : Asp Lys Val Gly Ly 170	
			CTG CAG GAC GAA CT Leu Gln Asp Glu Le 185	
		e Asp Arg Gly	TAC CTG TCT CCT TA Tyr Leu Ser Pro Ty 200	
			A TTG GAA AGC CCG TT Leu Glu Ser Pro Ph 215	
CTG CTG GCT GAC	AAG AAA AT	C TCC AAC ATO	C CGC GAA ATG CTG CC	G GTT 722

Leu Le	ı Ala	Asp	Lys 225	Lys	·Ile	Ser	Asn	Ile 230	Arg	Glu	Met	Leu	Pro 235	Val		
CTG GAA															770	
GAT GTT Asp Val															818	
GGT ATO	e Val														866	
CGT AAA Arg Lys 285															914	
ATC TC															962	
CTG GGG															1010 [:]	
ATC GAT															1058	·
ATT CGT Ile Arg	g Gln														1106	
CTG CAC Leu Glr 365															1154	
GTT GGT Val Gl _y															1202	
GAA GAT Glu Ası															1250	
GCT GGT Ala Gl _y															1298	
CTG AAA Leu Lys 430	Gly														1346	
CGC GCA Arg Ala															1394 -	

			GTA Val	Val				Lys					Asn		1442
			GCT Ala 480									Asp			1490
	Leu		CCA Pro				CGT								1538
	GTT	GCG	GGT Gly			ACC					GTT				1586
	AAA		GAT Asp		GAC					GGT					1634
ATG			ATG Met		ГСААС	GCC (SAATT	C	333					340	1665

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 545 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Ala Lys Asp Val Lys Phe Gly Asn Asp Ala Arg Val Lys Met
1 10 15

Leu Arg Gly Val Asn Val Leu Ala Asp Ala Val Lys Val Thr Leu Gly
20 25 30

Pro Lys Gly Arg Asn Val Val Leu Asp Lys Ser Phe Gly Ala Pro Thr 35 40 45

Ile Thr Lys Asp Gly Val Ser Val Ala Arg Glu Ile Glu Leu Glu Asp 50 55 60

Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Lys 65 70 75 80

Ala Asn Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala 85 90 95

Gln Ser Ile Ile Thr Glu Gly Leu Lys Ala Val Ala Ala Gly Met Asn 100 105 110

Pro	Met	Asp 115	Leu	Lys	Arg	Gly	Ile 120	Asp	Lys	Ala	Val	Ala 125	Ala	Ala	Val
Glu	Glu 130	Leu	Lys	Ala	Leu	Ser 135	Val	Pro	Cys	Ser	Asp 140	Ser	Lys	Ala	Ile
Ala 145	Gln	Val	Gly	Thr	Ile 150	Ser	Ala	Asn	Ser	Asp 155	Glu	Thr	Val	Gly	Lys 160
Leu	Ile	Ala	Glu	Ala 165	Met	Asp	Lys	Val	Gly 170	Lys	Glu	Gly	Val	Ile 175	Thr
Val	Glu	Asp	Gly 180	Thr	Gly	Leu	Gln	Asp 185	Glu	Leu	Asp	Val	Val 190	Glu	Gly
Met	Gln	Phe 195	Asp	Arg	Gly	Tyr	Leu 200	Ser	Pro	Tyr	Phe	Ile 205	Asn	Lys	Pro
Glu	Thr 210	Gly	Ala	Val	Glu	Leu 215	Glu	Ser	Pro	Phe	Ile 220	Leu	Leu	Ala	Asp
Lys 225	Lys	Ile	Ser	Asn	Ile 230	Arg	Glu	Met	Leu	Pro 235	Val	Leu	Glu	Ala	Val 240
Ala	Lys	Ala	Gly	Lys 245	Pro	Leu	Leu	Ile	Ile 250	Ala	Glu	Asp	Val	Glu 255	Gly
Glu	Ala	Leu	Ala 260	Thr	Leu	Val	Val	Asn 265	Thr	Met	Arg	Gly	Ile 270	Val	Lys
Val	Ala	Ala 275	Val	Lys	Ala	Pro	Gly 280	Phe	Gly	Asp	Arg	Arg 285	Lys	Ala	Met
Leu	Gln 290	Asp	Ile	Ala	Thr	Leu 295	Thr	Gly	Gly	Thr	Val 300	Ile	Ser	Glu	Glu
Ile 305	Gly	Met	Glu	Leu	Glu 310	Lys	Ala	Thr	Leu	Glu 315	Asp	Leu	Gly	Gln	Ala 320
Lys	Arg	Val	Val	Ile 325	Asn	Lys	Asp	Thr	Thr 330	Thr	Ile	Ile	Asp	Gly 335	Val
Gly	Asp	Glu	Ala 340	Ala	Ile	Gln	Gly	Arg 345	Val	Thr	Gln	Ile	Arg 350	Gln	Gln
Ile	Glu	Glu 355	Ala	Thr	Ser	Asp	Tyr 360	Asp	Arg	Glu	Lys	Leu 365	Gln	Glu	Arg
Val	Ala 370	Lys	Leu	Ala	Gly	Gly 375	Val	Ala	Val	Ile	Lys 380	Val	Gly	Ala	Ala
Thr 385	Glu	Val	Glu	Met	Lys 390	Glu	Lys	Lys	Ala	Arg 395	Val	Glu	Asp	Ala	Leu 400
His	Ala	Thr		Ala 405	Ala	Val	Glu	Glu	Gly 410	Val	Val	Ala	Gly	Gly 415	Gly

Val Ala Leu Ile Arg Val Ala Ser Lys Ile Ala Gly Leu Lys Gly Gln

420 425 430

Asn Glu Asp Gln Asn Val Gly Ile Lys Val Ala Leu Arg Ala Met Glu 435 440 Ser Pro Leu Arg Gln Ile Val Leu Asn Cys Gly Glu Glu Pro Ser Val 455 Val Ala Asn Thr Val Lys Ala Gly Asp Gly Asn Tyr Gly Tyr Asn Ala 470 475 Ala Thr Glu Glu Tyr Gly Asn Met Ile Asp Met Gly Ile Leu Asp Pro 490 Thr Lys Val Thr Arg Ser Ala Leu Gln Tyr Ala Ala Ser Val Ala Gly 505 Leu Met Ile Thr Thr Glu Cys Met Val Thr Asp Leu Pro Lys Gly Asp 515 520 Ala Pro Asp Leu Gly Ala Ala Gly Gly Met Gly Gly Met Gly Gly Met 535 540 Met 545 (2) INFORMATION FOR SEQ ID NO:3: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1654 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 15..1637 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: GAATTCGGCT TCAT ATG GCA AAA GAA ATT AAA TTT TCA TCA GAT GCC CGT 50 Met Ala Lys Glu Ile Lys Phe Ser Ser Asp Ala Arg TCA GCT ATG GTC CGT GGT GTC GAT ATC CTT GCA GAT ACT GTT AAA GTA 98 Ser Ala Met Val Arg Gly Val Asp Ile Leu Ala Asp Thr Val Lys Val ACT TTG GGA CCA AAA GGT CGC AAT GTC GTT CTT GAA AAG TCA TTC GGT 146 Thr Leu Gly Pro Lys Gly Arg Asn Val Val Leu Glu Lys Ser Phe Gly TCA CCC TTG ATT ACC AAT GAC GGT GTG ACT ATT GCC AAA GAA ATT GAA 194 Ser Pro Leu Ile Thr Asn Asp Gly Val Thr Ile Ala Lys Glu Ile Glu

55

45

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TTA GAA GA Leu Glu As												242
GCT TCA AM												290
GTT TTG AG Val Leu Th												338 .
GGT GCA AM Gly Ala As 110		le Gly										386
GCA GCA G Ala Ala Va 125												434
GAA GCT AT	le Ala G											482
GGT GAG TA												530
ATC ACC AT												.578
GAA GGA AT Glu Gly Me 190		he Asp A									-	626 ⁻
GAT AGC GA Asp Ser GI 205		ATG GTG (Met Val A 210									ATT Ile 220	674
ACA GAC AA Thr Asp Ly	ys Lys I											722
AGC ATT CT Ser Ile Le												770
GAT GGT GA Asp Gly Gl	lu Ala L											818
TTC AAC GT Phe Asn Va 270		la Val I						Asp				866
GCC ATG CT	TT GAA G	AT ATC	SCC ATC	TTA	ACA	GGC	GGA	ACA	GTT	ATC	ACA	914

Ala 285	Met	Leu	Glu	Asp	Ile 290	Ala	Ile	Leu	Thr	Gly 295	Gly	Thr	Val	Ile	Thr 300		
						TTG Leu										962	
						GTG Val										1010	
						GCG Ala										1058	
						ACT Thr 355										1106	
						TCA Ser										1154	
						TTG Leu										.1202	
						GCA Ala										1250	
						AAT Asn										1298	
						ACA Thr 435										1346	•
	GAA					ATT Ile										1394	
						AAA Lys										1442	
						GTT Val										1490	
			GTG			TCA Ser		CTA					тст			1538	
		ATT				GAA Glu 515	GCA					AAA				1586	

									AGT Ser							1634
GGA Gly	TGA:	ГСАА	AGC (CGÁA'	ГТС											1654
(2)	INF	ORMA'	rion	FOR	SEQ	I DI	NO:4	:								
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 541 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear(ii) MOLECULE TYPE: protein															
	(=	Li) N	MOLE	CULE	TYPI	E: pı	rote:	in								
	(2	ki) S	SEQUI	ENCE	DES	CRIP:	rion	: SE	Q ID	NO:	1:					
Met 1	Ala	Lys	Glu	Ile 5	Lys	Phe	Ser	Ser	Asp 10	Ala	Arg	Ser	Ala	Met 15	Val	
Arg	Gly	Val	Asp 20	Ile	Leu	Ala	Asp	Thr 25	Val	Lys	Val	Thr	Leu 30	Gly	Pro	
Lys	Gly	Arg 35	Asn	Val	Val	Leu	Glu 40	Lys	Ser	Phe	Gly	Ser 45	Pro	Leu	Ile	
Thr	Asn 50	Asp	Gly	Val	Thr	Ile 55	Ala	Lys	Glu	Ile	Glu 60	Leu	Glu	Asp	His	
Phe 65	Glu	Asn	Met	Gly	Ala 70	Lys	Leu	Val	Ser	Glu 75	Val	Ala	Ser	Lys	Thr 80	
Asn	Asp	Ile	Ala	Gly 85	Asp	Gly	Thr	Thr	Thr 90	Ala	Thr	Val	Leu	Thr 95	Gln	
Ala	Ile	Val	Arg 100	Glu	Gly	Ile	Lys	Asn 105	Val	Thr	Ala	Gly	Ala 110	Asn	Pro	
Ile	Gly	Ile 115	Arg	Arg	Gly	Ile	Glu 120	Thr	Ala	Val	Ala	Ala 125	Ala	Val	Glu	
Ala	Leu 130	Lys	Asn	Asn	Val	Ile 135	Pro	Val	Ala	Asn	Lys 140	Glu	Ala	Ile	Ala	
Gln 145	Val	Ala	Ala	Val	Ser 150	Ser	Arg	Ser	Glu	Lys 155	Val	Gly	Glu	Tyr	Ile 160	
Ser	Glu	Ala	Met	Glu 165	Lys	Val	Gly	Lys	Asp 170	Gly	Val	Ile	Thr	Ile 175	Glu	
Glu	Ser	Arg	Gly 180	Met	Glu	Thr	Glu	Leu 185	Glu	Val	Val	Glu	Gly 190	Met	Gln	
Phe	Asp	Arg	Gly	Tyr	Leu	Ser	Gln	Tyr	Met	Val	Thr	Asp	Ser	Glu	Lys	

195 200 205

Met	Val 210	Ala	Asp	Leu	Glu	Asn 215	Pro	Tyr	Ile	Leu	Ile 220	Thr	Asp	Lys	Lys
Ile 225	Ser	Asn	Ile	Gln	Glu 230	Ile	Leu	Pro	Leu	Leu 235	Glu	Ser	Ile	Leu	Glr 240
Ser	Asn	Arg	Pro	Leu 245	Leu	Ile	Ile	Ala	Asp 250	Asp	Val	Asp	Gly	Glu 255	Alá
Leu	Pro	Thr	Leu 260	Val	Leu	Asn	Lys	Ile 265	Arg	Gly	Thr	Phe	Asn 270	Val	Val
Ala	Val	Lys 275	Ala	Pro	Gly	Phe	Gly 280	Asp	Arg	Arg	Lys	Ala 285	Met	Leu	Glu
Asp	Ile 290	Ala	Ile	Leu	Thr	Gly 295	Gly	Thr	Val	Ile	Thr 300	Glu	Asp	Leu	GlΣ
Leu 305	Glu	Leu	Lys	Asp	Ala 310	Thr	Ile	Glu	Ala	Leu 315	Gly	Gln	Ala	Ala	Arg 320
Val	Thr	Val	Asp	Lys 325	Asp	Ser	Thr	Val	Ile 330	Val	Glu	Gly	Ala	Gly 335	Asr
Pro	Glu	Ala	Ile 340	Ser	His	Arg	Val	Ala 345	Val	Ile	Lys	Ser	Gln 350	Ile	Glu
Thr	Thr	Thr 355	Ser	Glu	Phe	Asp	Arg 360	Glu	Lys	Leu	Gln	Glu 365	Arg	Leu	Ala
Lys	Leu 370	Ser	Gly	Gly	Val	Ala 375	Val	Ile	Lys	Val	Gly 380	Ala	Ala	Thr	Glu
Thr 385	Glu	Leu	Lys	Glu	Met 390	Lys	Leu	Arg	Ile	Glu 395	Asp	Ala	Leu	Asn	Ala 400
Thr	Arg	Ala	Ala	Val 405	Glu	Glu	Gly	Ile	Val 410	Ala	Gly	Gly	Gly	Thr 415	Ala
Leu	Ala	Asn	Val 420	Ile	Pro	Ala	Val	Ala 425	Thr	Leu	Glu	Leu	Thr 430	Gly	Asp
Glu	Ala	Thr 435	Gly	Arg	Asn	Ile	Val 440	Leu	Arg	Ala	Leu	Glu 445	Glu	Pro	Va]
Arg	Gln 450	Ile	Ala	His	Asn	Ala 455	Gly	Phe	Glu	Gly	Ser 460	Ile	Val	Ile	Asp
Arg 465	Leu	Lys	Asn	Ala	Glu 470	Leu	Gly	Ile	Gly	Phe 475	Asn	Ala	Ala	Thr	Gl _y 480
Glu	Trp	Val	Asn	Met 485	Ile	Asp	Gln	Gly	Ile 490	Ile	Asp	Pro	Val	Lys 495	Val
Ser	Arg	Ser	Ala		Gln	Asn	Ala	Ala		Val	Ala	Ser	Leu 510		Leu

Thr Thr Glu Ala Val Val Ala Asn Lys Pro Glu Pro Val Ala Pro Ala 515 520 525

Pro Ala Met Asp Pro Ser Met Met Gly Gly Met Gly Gly 530 535 540

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1662 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 15..1646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCGGCT TCAT		AAA TTC GGT AAC Lys Phe Gly Asn 10	
		CTG GCA GAC GCA Leu Ala Asp Ala 25	
	Arg Asn Val	GTG CTG GAC AAA Val Leu Asp Lys 40	
		TCT GTA GCA CGT Ser Val Ala Arg 55	
		GCG CAG ATG GTG Ala Gln Met Val	
		GAC GGT ACC ACC Asp Gly Thr Thr 90	
		GGT CTG AAA GCC Gly Leu Lys Ala 105	
		GGT ATC GAC AAA Gly Ile Asp Lys 120	
		TCC GTA CCG TGC Ser Val Pro Cys	

125			130			135			140	
								GAC Asp 155		482
								AAA Lys		530
								CTG Leu		578
								TAC Tyr		626
								TTC Phe		674
	-							CCA Pro 235		722
								GCT Ala		770
								ATG Met		818
								GAC Asp		866
								ACC Thr		914
								GAA Glu 315		962
								ACC Thr		1010
								GGT Gly		1058
								GAA Glu		1106

							GGC Gly				1154
							AAA Lys 390				1202
							GCG Ala				1250
							GTT Val				1298
							GTG Val				1346
							ATC Ile				1394
							AAA Lys 470				1442
							GGC Gly			_	1490
							TCT Ser				1538
-							GAG Glu				1586
							GCT Ala				1634
	ATG Met	TGAT	ГСААС	GCC C	TAAT	rc					1662

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 544 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

- Met Ala Ala Lys Asp Val Lys Phe Gly Asn Asp Ala Arg Val Lys Met

 1 5 10 15

 Leu Arg Gly Val Asn Val Leu Ala Asp Ala Val Lys Val Thr Leu Gly
- Pro Lys Gly Arg Asn Val Val Leu Asp Lys Ser Phe Gly Ala Pro Thr
- Ile Thr Lys Asp Gly Val Ser Val Ala Arg Glu Ile Glu Leu Glu Asp
- Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Lys 65 70 75 80
- Ala Asn Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala
- Gln Ala Ile Ile Thr Glu Gly Leu Lys Ala Val Ala Ala Gly Met Asn 100 105 110
- Pro Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Val Ala Ser Ala Val
 115 120 125
- Glu Glu Leu Lys Ala Leu Ser Val Pro Cys Ser Asp Ser Lys Ala Ile 130 135 140
- Ala Gln Val Gly Thr Ile Ser Ala Asn Ser Asp Glu Thr Val Gly Lys 145 150 155 160
- Leu Ile Ala Glu Ala Met Asp Lys Val Gly Lys Glu Gly Val Ile Thr
 165 170 175
- Val Glu Asp Gly Thr Gly Leu Glu Asp Glu Leu Asp Val Val Glu Gly 180 185 190
- Met Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Ile Asn Lys Pro 195 200 205
- Glu Thr Gly Ala Val Glu Leu Glu Ser Pro Phe Ile Leu Leu Ala Asp 210 215 220
- Lys Lys Ile Ser Asn Ile Arg Glu Met Leu Pro Val Leu Glu Ala Val 225 230 235 240
- Ala Lys Ala Gly Lys Pro Leu Val Ile Ile Ala Glu Asp Val Glu Gly 245 250 255
- Glu Ala Leu Ala Thr Leu Val Val Asn Thr Met Arg Gly Ile Val Lys
 260 265 270
- Val Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met 275 280 285
- Leu Gln Asp Ile Ala Thr Leu Thr Gly Gly Thr Val Ile Ser Glu Glu 290 295 300

Ile Gly Met Glu Leu Glu Lys Ala Thr Leu Glu Asp Leu Gly Gln Ala 305 310 315 320

Lys Arg Val Val Ile Asn Lys Asp Thr Thr Ile Ile Asp Gly Val
325 330 335

Gly Asp Glu Ala Ala Ile Gln Gly Arg Val Gly Gln Ile Arg Lys Gln 340 345 350

Ile Glu Glu Ala Thr Ser Asp Tyr Asp Arg Glu Lys Leu Gln Glu Arg 355 360 365

Thr Glu Val Glu Met Lys Glu Lys Lys Ala Arg Val Asp Asp Ala Leu 385 390 395 400

His Ala Thr Arg Ala Ala Val Glu Glu Gly Val Val Ala Gly Gly Gly 405 410 415

Val Ala Leu Val Arg Val Ala Ala Lys Leu Ser Gly Leu Thr Ala Gln 420 425 430

Asn Glu Asp Gln Asn Val Gly Ile Lys Val Ala Leu Arg Ala Met Glu 435 440 445

Ala Pro Leu Arg Gln Ile Val Ser Asn Ala Gly Glu Glu Pro Ser Val 450 455 460

Val Thr Asn Asn Val Lys Ala Gly Glu Gly Asn Tyr Gly Tyr Asn Ala 465 470 475 480

Ala Thr Glu Glu Tyr Gly Asn Met Ile Asp Phe Gly Ile Leu Asp Pro 485 490 495

Thr Lys Val Thr Arg Ser Ala Leu Gln Tyr Ala Ala Ser Val Ala Gly 500 505 510

Leu Met Ile Thr Thr Glu Cys Met Val Thr Asp Leu Pro Lys Gly Asp 515 520 525

Ala Pro Asp Leu Gly Ala Ala Gly Met Gly Gly Met Gly Gly Met Met 530 535 540

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1661 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 15..1649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAA.	rtcg(GCT '	TCAT	ATG Met 1					AAA Lys							50
				CGC Arg												98
				AAA Lys												146
				ACT Thr												194
				TTT Phe 65												242
				AAT Asn												290
				GCC Ala												338
				ATT Ile												386
				GCC Ala												434
				CAG Gln 145												482
				TCA Ser												530
				GAA Glu												578
				TTT Phe												626
GAC	AAT	GAA	AAA	ATG	GTT	GCA	GAC	CTT	GAA	AAC	CCA	TTT	ATC	TTA	ATC	674

											_			_			
Asp 205	Asn	Glu	Lys	Met	Val 210	Ala	Asp	Leu	Glu	Asn 215	Pro	Phe	Ile	Leu	11e 220		
	GAT Asp															722	
	GTT Val															770	
	GGT Gly															818	
	AAT Asn 270	Val														866	
	ATG Met															914	
	GAT Asp															962	
	GCT Ala															1010	
	TCA Ser															1058	•
	CAA Gln 350															1106	
	CGT Arg															1154	
	CCA Pro															1202	
	CTA Leu															1250	
	GGA Gly															1298	
	GAG Glu 430															1346	

						ATT Ile										1394
						AAA Lys										1442
						GTT Val										1490
						TCA Ser										1538
						GAA Glu 515										1586
						ATG Met										1634
	GGG Gly				TAAC	GCCG <i>I</i>	AAT T	rc								1661
(2)	INFO)RMAT	rion	FOR	SEQ	ID N	10:8:									
	(2) INFORMATION FOR SEQ ID NO:8: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 545 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear															
	(i	.i) N	OLEC	CULE	TYPE	E: pr	otei	.n								
	(2	xi) S	SEQUE	ENCE	DESC	CRIPT	CION:	SEÇ) ID	NO:8	3:					
Met 1	Ala	Lys	Glu	Ile 5	Lys	Phe	Ser	Ala	Asp 10	Ala	Arg	Ala	Ala	Met 15	Val	

Arg Gly Val Asp Met Leu Ala Asp Thr Val Lys Val Thr Leu Gly Pro 25

Lys Gly Arg Asn Val Val Leu Glu Lys Ala Phe Gly Ser Pro Leu Ile 40

Thr Asn Asp Gly Val Thr Ile Ala Lys Glu Ile Glu Leu Glu Asp His

Phe Glu Asn Met Gly Ala Lys Leu Val Ser Glu Val Ala Ser Lys Thr

Asn Asp Ile Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Thr Gln

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- Ala Ile Val His Glu Gly Leu Lys Asn Val Thr Ala Gly Ala Asn Pro 100 105 110
- Ile Gly Ile Arg Arg Gly Ile Glu Thr Ala Thr Ala Thr Ala Val Glu
 115 120 125
- Ala Leu Lys Ala Ile Ala Gln Pro Val Ser Gly Lys Glu Ala Ile Ala 130 135 140
- Gln Val Ala Ala Val Ser Ser Arg Ser Glu Lys Val Gly Glu Tyr Ile 145 150 155 160
- Ser Glu Ala Met Glu Arg Val Gly Asn Asp Gly Val Ile Thr Ile Glu 165 170 175
- Glu Ser Arg Gly Met Glu Thr Glu Leu Glu Val Val Glu Gly Met Gln 180 185 190
- Phe Asp Arg Gly Tyr Leu Ser Gln Tyr Met Val Thr Asp Asn Glu Lys 195 200 205
- Met Val Ala Asp Leu Glu Asn Pro Phe Ile Leu Ile Thr Asp Lys Lys 210 215 220
- Val Ser Asn Ile Gln Asp Ile Leu Pro Leu Leu Glu Glu Val Leu Lys 225 230 235 240
- Thr Asn Arg Pro Leu Leu Ile Ile Ala Asp Asp Val Asp Gly Glu Ala
 245 250 255
- Leu Pro Thr Leu Val Leu Asn Lys Ile Arg Gly Thr Phe Asn Val Val 260 265 270
- Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Lys Ala Met Leu Glu 275 280 285

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- Asp Ile Ala Ile Leu Thr Gly Gly Thr Val Ile Thr Glu Asp Leu Gly 290 295 300
- Leu Glu Leu Lys Asp Ala Thr Met Thr Ala Leu Gly Gln Ala Ala Lys 305 310 315 320
- Ile Thr Val Asp Lys Asp Ser Thr Val Ile Val Glu Gly Ser Gly Ser 325 330 335
- Ser Glu Ala Ile Ala Asn Arg Ile Ala Leu Ile Lys Ser Gln Leu Glu 340 345 350
- Thr Thr Ser Asp Phe Asp Arg Glu Lys Leu Gln Glu Arg Leu Ala 355 360 365
- Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Pro Thr Glu 370 375 380
- Thr Ala Leu Lys Glu Met Lys Leu Arg Ile Glu Asp Ala Leu Asn Ala 385 390 395 400

Thr Arg Ala Ala Val Glu Glu Gly Ile Val Ala Gly Gly Gly Thr Ala
405 410 415

Leu Ile Thr Val Ile Glu Lys Val Ala Ala Leu Glu Leu Glu Gly Asp 420 425 430

Asp Ala Thr Gly Arg Asn Ile Val Leu Arg Ala Leu Glu Glu Pro Val 435 440 445

Arg Gln Ile Ala Leu Asn Ala Gly Tyr Glu Gly Ser Val Val Ile Asp 450 455 460

Lys Leu Lys Asn Ser Pro Ala Gly Thr Gly Phe Asn Ala Ala Thr Gly 465 470 475 480

Glu Trp Val Asp Met Ile Lys Thr Gly Ile Ile Asp Pro Val Lys Val
485 490 495

Thr Arg Ser Ala Leu Gln Asn Ala Ala Ser Val Ala Ser Leu Ile Leu 500 505 510

Thr Thr Glu Ala Val Val Ala Asn Lys Pro Glu Pro Ala Thr Pro Ala 515 520 525

Pro Ala Met Pro Ala Gly Met Asp Pro Gly Met Met Gly Gly Met Gly 530 535 540

Gly 545

- (2) INFORMATION FOR SEQ ID NO:9:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 544 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Lys Glu Ile Lys Phe Ser Glu Glu Ala Arg Arg Ala Met Leu 1 5 10 15

Arg Gly Val Asp Ala Leu Ala Asp Ala Val Lys Val Thr Leu Gly Pro 20 25 30

Lys Gly Arg Asn Val Val Leu Glu Lys Lys Phe Gly Ser Pro Leu Ile $35 \hspace{1cm} 40 \hspace{1cm} 45$

Thr Asn Asp Gly Val Thr Ile Ala Lys Glu Ile Glu Leu Glu Asp Ala 50 55 60

Phe Glu Asn Met Gly Ala Lys Leu Val Ala Glu Val Ala Ser Lys Thr 70 75 80

- Asn Asp Val Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Gln 85 90 95
- Ala Met Ile Arg Glu Gly Leu Lys Asn Val Thr Ala Gly Ala Asn Pro 100 105 110
- Val Gly Val Arg Lys Gly Met Glu Gln Ala Val Ala Val Ala Ile Glu 115 120 125
- Asn Leu Lys Glu Ile Ser Lys Pro Ile Glu Gly Lys Glu Ser Ile Ala 130 135 140
- Gln Val Ala Ala Ile Ser Ala Ala Asp Glu Glu Val Gly Ser Leu Ile 145 150 155 160
- Ala Glu Ala Met Glu Arg Val Gly Asn Asp Gly Val Ile Thr Ile Glu 165 170 175
- Glu Ser Lys Gly Phe Thr Thr Glu Leu Glu Val Val Glu Gly Met Gln 180 185 190
- Phe Asp Arg Gly Tyr Ala Ser Pro Tyr Met Val Thr Asp Ser Asp Lys 195 200 205
- Met Glu Ala Val Leu Asp Asn Pro Tyr Ile Leu Ile Thr Asp Lys Lys 210 215 220
- Ile Thr Asn Ile Glu Glu Ile Leu Pro Val Leu Glu Gln Val Val Gln 225 230 235 . 240
- Gln Gly Lys Pro Leu Leu Ile Ala Glu Asp Val Glu Gly Glu Ala 245 250 255
- Leu Ala Thr Leu Val Val Asn Lys Leu Arg Gly Thr Phe Asn Ala Val 260 265 270
- Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met Leu Glu 275 280 285
- Asp Ile Ala Val Leu Thr Gly Gly Glu Val Ile Thr Glu Asp Leu Gly 290 295 300
- Leu Asp Leu Lys Ser Thr Gln Ile Ala Gln Leu Gly Arg Ala Ser Lys 305 310 315 320
- Val Val Val Thr Lys Glu Asn Thr Thr Ile Val Glu Gly Ala Gly Glu 325 330 335
- Thr Asp Lys Ile Ser Ala Arg Val Thr Gln Ile Arg Ala Gln Val Glu 340 345 350
- Glu Thr Thr Ser Glu Phe Asp Arg Glu Lys Leu Gln Glu Arg Leu Ala 355 360 365
- Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala Thr Glu 370 375 380

Thr Glu Leu Lys Glu Arg Lys Leu Arg Ile Glu Asp Ala Leu Asn Ser 385 390 395 400

Thr Arg Ala Ala Val Glu Glu Gly Ile Val Ser Gly Gly Gly Thr Ala 405 410 415

Leu Val Asn Val Tyr Asn Lys Val Ala Ala Val Glu Ala Glu Gly Asp
420 425 430

Ala Gln Thr Gly Ile Asn Ile Val Leu Arg Ala Leu Glu Glu Pro Ile 435 440 445

Arg Gln Ile Ala His Asn Ala Gly Leu Glu Gly Ser Val Ile Val Glu 450 455 460

Arg Leu Lys Asn Glu Glu Ile Gly Val Gly Phe Asn Ala Ala Thr Gly 465 470 475 480

Glu Trp Val Asn Met Ile Glu Lys Gly Ile Val Asp Pro Thr Lys Val 485 490 495

Thr Arg Ser Ala Leu Gln Asn Ala Ala Ser Val Ala Ala Met Phe Leu 500 505 510

Thr Thr Glu Ala Val Val Ala Asp Lys Pro Glu Glu Asn Gly Gly 515 520 525

Ala Gly Met Pro Asp Met Gly Gly Met Gly Gly Met Met 530 535 540

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 539 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ala Lys Thr Leu Leu Phe Gly Glu Glu Ala Arg Arg Ser Met Gln 1 5 10 15

Ala Gly Val Asp Lys Leu Ala Asn Thr Val Lys Val Thr Leu Gly Pro 20 25 30

Lys Gly Arg Asn Val Ile Leu Asp Lys Lys Phe Gly Ser Pro Leu Ile 35 . 40 45

Thr Asn Asp Gly Val Thr Ile Ala Arg Glu Ile Glu Leu Glu Asp Ala 50 55 60

Tyr Glu Asn Met Gly Ala Gln Leu Val Lys Glu Val Ala Thr Lys Thr

65 70 75 80

Asn Asp Val Ala Gly Asp Gly Thr Thr Thr Ala Thr Leu Leu Ala Gln 90 Ala Ile Ile Arg Glu Gly Leu Lys Asn Val Thr Ala Gly Ala Asn Pro 105 Ile Leu Ile Arg Asn Gly Ile Lys Thr Ala Val Glu Lys Ala Val Glu 120 Glu Ile Gln Lys Ile Ser Lys Pro Val Asn Gly Lys Glu Asp Ile Ala 135 Arg Val Ala Ala Ile Ser Ala Ala Asp Glu Lys Ile Gly Lys Leu Ile 150 Ala Asp Ala Met Glu Lys Val Gly Asn Glu Gly Val Ile Thr Val Glu Glu Ser Lys Ser Met Gly Thr Glu Leu Asp Val Val Glu Gly Met Gln 185 Phe Asp Arg Gly Tyr Val Ser Ala Tyr Met Val Thr Asp Thr Glu Lys 200 Met Glu Ala Val Leu Asp Asn Pro Leu Val Leu Ile Thr Asp Lys Lys 215 Ile Ser Asn Ile Gln Asp Leu Leu Pro Leu Leu Glu Gln Ile Val Gln 230 235 Ala Gly Lys Lys Leu Leu Ile Ile Ala Asp Asp Ile Glu Gly Glu Ala 245 250 Met Thr Thr Leu Val Val Asn Lys Leu Arg Gly Thr Phe Thr Cys Val Gly Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Glu Met Leu Gln 280 285 275 Asp Ile Ala Thr Leu Thr Gly Gly Val Val Ile Ser Asp Glu Val Gly Gly Asp Leu Lys Glu Ala Thr Leu Asp Met Leu Gly Glu Ala Glu Ser 310 315 Val Lys Val Thr Lys Glu Ser Thr Thr Ile Val Asn Gly Arg Gly Asn 325 330 Ser Glu Glu Ile Lys Asn Arg Ile Asn Gln Ile Lys Leu Gln Leu Glu 345 Ala Thr Thr Ser Glu Phe Asp Lys Glu Lys Leu Gln Glu Arg Leu Ala 355 360 365 Lys Leu Ala Gly Gly Val Ala Val Val Lys Val Gly Ala Ala Thr Glu

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Thr Glu Leu Lys Glu Ser Lys Leu Arg Ile Glu Asp Ala Leu Ala Ala 385 390 395 400

Thr Lys Ala Ala Val Glu Glu Gly Ile Val Pro Gly Gly Gly Thr Ala
405 410 415

Tyr Val Asn Val Ile Asn Glu Val Ala Lys Leu Thr Ser Asp Ile Gln 420 425 430

Asp Glu Gln Val Gly Ile Asn Ile Ile Val Arg Ser Leu Glu Glu Pro 435 440 445

Met Arg Gln Ile Ala His Asn Ala Gly Leu Glu Gly Ser Val Ile Ile 450 455 460

Glu Lys Val Lys Asn Ser Asp Ala Gly Val Gly Phe Asp Ala Leu Arg 465 470 475 480

Gly Glu Tyr Lys Asp Met Ile Lys Ala Gly Ile Val Asp Pro Thr Lys 485 490 495

Val Thr Arg Ser Ala Leu Gln Asn Ala Ala Ser Val Ala Ser Thr Phe 500 505 510

Leu Thr Thr Glu Ala Ala Val Ala Asp Ile Pro Glu Lys Glu Met Pro 515 520 525

Gln Gly Ala Gly Met Gly Met Asp Gly Met Tyr 530 535

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 551 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Glu Val Val Arg Ile Leu Glu Asp Ala Val Gly Cys Thr Ala Gly Pro $20 \hspace{1cm} 25 \hspace{1cm} 30$

Lys Gly Leu Thr Val Ala Ile Ser Lys Pro Tyr Gly Ala Pro Glu Val 35 40 45

Thr Lys Asp Gly Tyr Lys Val Met Lys Ser Ile Lys Pro Glu Asp Pro 50 55 60

Leu Ala Leu Ala Ile Ala Asn Ile Ile Ala Gln Ser Ala Ser Gln Cys

Asn Asp Lys Val Gly Asp Gly Thr Thr Thr Cys Ser Ile Leu Thr Ala Lys Val Ile Glu Glu Val Ser Lys Val Lys Ala Ala Gly Ala Asp Ile Ile Cys Val Arg Glu Gly Val Leu Lys Ala Lys Glu Ala Val Leu Glu Ala Leu Lys Cys Met Lys Arg Glu Val Leu Ser Glu Glu Glu Ile Ala Gln Val Ala Thr Ile Ser Ala Asn Gly Asp Lys Asn Ile Gly Thr Lys Ile Ala Gln Cys Val Lys Glu Val Gly Lys Asp Gly Val Ile Thr Val Glu Glu Ser Lys Gly Phe Lys Glu Leu Asp Val Glu Lys Thr Asp Gly Met Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Val Thr Asn Ser Glu Lys Met Leu Val Glu Phe Glu Asn Pro Tyr Ile Leu Leu Thr Glu Lys Lys Leu Asn Ile Ile Gln Pro Leu Leu Pro Ile Leu Glu Asn Ile Ala Arg Ser Gly Arg Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly Glu Ala Leu Ser Thr Leu Val Leu Asn Lys Leu Arg Gly Gly Leu His Val Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Asp Met Leu Gly Asp Ile Ala Ile Leu Thr Gly Ala Lys His Val Ile Asn Asp Glu Leu Ala Ile Lys Met Glu Asp Leu Thr Leu Cys Asp Leu Gly Thr Ala Lys Asn Ile Arg Ile Thr Lys Asp Thr Thr Thr Ile Ile Gly Ser Val Asp Asn Ser Cys Ala His Val Gln Ser Arg Ile Cys Gln Ile Arg Met Gln Ile Asp Asn Ser Thr Ser Asp Tyr Asp Lys Glu Lys Leu Gln Glu Arg Leu Ala Lys Leu Ser Gly Gly Val Ala Val Leu Lys Val Gly

Gly Ser Ser Glu Val Glu Val Lys Glu Arg Lys Asp Arg Val Glu Asp 385 390 395 400

Ala Leu His Ala Thr Arg Ala Ala Val Glu Glu Gly Val Val Pro Gly
405 410 415

Gly Gly Ala Ala Leu Leu Tyr Thr Leu Ser Ala Leu Asp Asn Leu Lys
420 425 430

Ser Lys Asn Asp Asp Glu Gln Leu Gly Ile Asn Ile Val Lys Arg Ala 435 440 445

Leu Gln Ala Pro Ile Lys Arg Ile Ile Lys Asn Ala Gly Ser Glu Asn 450 455 460

Ala Pro Cys Val Ile Ala His Leu Leu Lys Gln Asn Asp Lys Glu Leu 465 470 475 480

Ile Phe Asn Val Asp Val Thr Asn Phe Ala Asn Ala Phe Thr Ser Gly 485 490 495

Val Ile Asp Pro Leu Lys Val Val Arg Ile Ala Phe Asp Phe Ala Val 500 505 510

Ser Leu Ala Ala Val Phe Met Thr Leu Asn Ala Ile Val Val Asp Ile 515 520 525

Pro Ser Lys Asp Asp Asn Ser Ala Ala Gly Gly Ala Gly Met Gly Gly 530 540

Met Gly Gly Met Gly Gly Phe 545 550

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 548 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Ala Ala Lys Asp Val Lys Phe Gly Asn Asp Ala Arg Val Lys Met 1 5101510

Leu Asn Gly Val Asn Ile Leu Ala Asp Ala Val Lys Val Thr Leu Gly 20 25 30

Pro Lys Gly Arg Asn Val Val Leu Asp Lys Ser Phe Gly Ala Pro Thr 35 40 45

Ile Thr Lys Asp Gly Val Ser Val Ala Arg Glu Ile Glu Leu Glu Asp

Lys 65	Phe	Glu	Asn	Met	Gly 70	Ala	Gln	Met	Val	Lys 75	Glu	Val	Ala	Ser	Lys 80
Ala	Asn	Asp	Ala	Ala 85	Gly	Asp	Gly	Thr	Thr 90	Thr	Ala	Thr	Val	Leu 95	Ala
Gln	Ala	Ile	Val 100	Asn	Glu	Gly	Leu	Lys 105	Ala	Val	Ala	Ala	Gly 110	Met	Asn
Pro	Met	Asp 115	Leu	Lys	Arg	Gly	Ile 120	Asp	Lys	Ala	Val	Asn 125	Ser	Val	Val
Ala	Glu 130	Leu	Lys	Asn	Leu	Ser 135	Lys	Pro	Cys	Glu	Thr 140	Ser	Lys	Glu	Ile
Glu 145	Gln	Val	Gly	Thr	Ile 150	Ser	Ala	Asn	Ser	Asp 155	Ser	Ile	Val	Gly	Gln 160
Leu	Ile	Ala	Gln	Ala 165	Met	Glu	Lys	Val	Gly 170	Lys	Glu	Gly	Val	Ile 175	Thr
Val	Glu	Asp	Gly 180	Thr	Gly	Leu	Glu	Asp 185	Glu	Leu	Asp	Val	Val 190	Glu	Gly
Met	Gln	Phe 195	Asp	Arg	Gly	Tyr	Leu 200	Ser	Pro	Tyr	Phe	Ile 205	Asn	Lys	Pro
Glu	Thr 210	Ala	Gly	Thr	Val	Glu 215	Leu	Asp	Asn	Pro	Phe 220	Ile	Leu	Leu	Val
Asp 225	Lys	Lys	Ile	Ser	Asn 230	Ile	Arg	Glu	Leu	Leu 235	Pro	Val	Leu	Glu	Ala 240
Val	Ala	Lys	Ala	Gly 245	Lys	Pro	Leu	Leu	Ile 250	Ile	Ala	Glu	Asp	Val 255	Glu
Gly	Glu	Ala	Leu 260	Ala	Thr	Leu	Val	Val 265	Asn	Thr	Met	Arg	Gly 270	Ile	Val
Lys	Val	Ala 275	Ala	Val	Lys	Ala	Pro 280	Gly	Phe	Gly	Asp	Arg 285	Arg	Lys	Ala
Met	Leu 290	Gln	Asp	Ile	Ala	Ile 295	Leu	Thr	Ala	Gly	Thr 300	Val	Ile	Ser	Glu
Glu 305	Ile	Gly	Met	Glu	Leu 310	Glu	Lys	Ala	Thr	Leu 315	Glu	Glu	Leu	Gly	Gln 320
Ala	Lys	Arg	Val	Val 325	Ile	Thr	Lys	Asp	Asn 330	Thr	Thr	Ile	Ile	Asp 335	Gly
Ile	Gly	Asp	Glu 340	Ala	Gln	Ile	Lys	Ala 345	Arg	Val	Val	Gln	Ile 350	Arg	Gln
Gln	Ile	Glu 355	Asp	Ser	Thr	Ser	Asp 360	Tyr	Asp	Lys	Glu	Lys 365	Leu	Gln	Glu

- Arg Val Ala Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala 370 380
- Ala Thr Glu Val Ala Met Lys Glu Lys Lys Asp Arg Val Asp Asp Ala 385 390 395 400
- Leu His Ala Thr Arg Ala Ala Val Glu Glu Gly Ile Val Pro Gly Gly 405 410 415
- Gly Val Ala Leu Val Arg Ala Ala Asn Lys Val Ser Ala Thr Leu Thr 420 425 430
- Gly Asp Asn Glu Glu Gln Asn Val Gly Ile Lys Leu Ala Leu Arg Ala 435 440 445
- Met Glu Ala Pro Leu Arg Gln Ile Val Glu Asn Ser Gly Glu Asp Ala 450 455 460
- Ser Val Val Ala Arg Asp Val Lys Asp Gly Ser Gly Asn Phe Gly Tyr 465 470 475 480
- Asn Ala Thr Thr Glu Glu Tyr Gly Asp Met Leu Glu Met Gly Ile Leu 485 490 495
- Asp Pro Thr Lys Val Thr Arg Ser Ala Leu Gln Phe Ala Ala Ser Ile 500 505 510
- Ala Gly Leu Met Ile Thr Thr Glu Cys Met Ile Thr Asp Leu Pro Lys 515 520 525
- Glu Asp Lys Leu Asp Ala Gln Ala Ala Met Gly Gly Met Gly Gly Met 530 535 540

Gly Gly Met Met 545

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 549 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

- Met Ala Lys Glu Leu Arg Phe Gly Asp Asp Ala Arg Leu Gln Met Leu 1 5 10 15
- Ala Gly Val Asn Ala Leu Ala Asp Ala Val Gln Val Thr Met Gly Pro 20 25 30
- Arg Gly Arg Asn Val Val Leu Glu Lys Ser Tyr Gly Ala Pro Thr Val

Thr Lys Asp Gly Val Ser Val Ala Lys Glu Ile Glu Phe Glu His Arg Phe Met Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Lys Thr Ser Asp Thr Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Arg 90 Ser Ile Leu Val Glu Gly His Lys Ala Val Ala Ala Gly Met Asn Pro 100 105 Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Val Leu Ala Val Thr Lys Lys Leu Gln Ala Met Ser Lys Pro Cys Lys Asp Ser Lys Ala Ile Ala 135 Gln Val Gly Thr Ile Ser Ala Asn Ser Asp Glu Ala Ile Gly Ala Ile 150 155 Ile Ala Glu Ala Met Glu Lys Val Gly Lys Glu Gly Val Ile Thr Val 170 Glu Asp Gly Asn Gly Leu Glu Asn Glu Leu Ser Val Val Glu Gly Met 185 Gln Phe Asp Arg Gly Tyr Ile Ser Pro Tyr Phe Ile Asn Asn Gln Gln 200 Asn Met Ser Cys Glu Leu Glu His Pro Phe Ile Leu Leu Val Asp Lys 210 215 Lys Val Ser Ser Ile Arg Glu Met Leu Ser Val Leu Glu Gly Val Ala 230 235 Lys Ser Gly Arg Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly Glu 245 250 Ala Leu Ala Thr Leu Val Val Asn Asn Met Arg Gly Ile Val Lys Val 265 Cys Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met Leu 280 Gln Asp Ile Ala Ile Leu Thr Lys Gly Gln Val Ile Ser Glu Glu Ile 290 295 Gly Lys Ser Leu Glu Gly Ala Thr Leu Glu Asp Leu Gly Ser Ala Lys 310 315 Arg Ile Val Val Thr Lys Glu Asn Thr Thr Ile Ile Asp Gly Glu Gly 325 330 335 Lys Ala Thr Glu Ile Asn Ala Arg Ile Thr Gln Ile Arg Ala Gln Met 340 345

- Glu Glu Thr Thr Ser Asp Tyr Asp Arg Glu Lys Leu Gln Glu Arg Val 355 360 365
- Ala Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala Thr 370 375 380
- Glu Val Glu Met Lys Glu Lys Lys Ala Arg Val Glu Asp Ala Leu His 385 390 395 400
- Ala Thr Arg Ala Ala Val Glu Glu Gly Ile Val Ala Gly Gly Val 405 410 415
- Ala Leu Ile Arg Ala Gln Lys Ala Leu Asp Ser Leu Lys Gly Asp Asn 420 425 430
- Asp Asp Gln Asn Met Gly Ile Asn Ile Leu Arg Arg Ala Ile Glu Ser 435 440 445
- Pro Met Arg Gln Ile Val Thr Asn Ala Gly Tyr Glu Ala Ser Val Val 450 455 460
- Val Asn Lys Val Ala Glu His Lys Asp Asn Tyr Gly Phe Asn Ala Ala 465 470 475 480
- Thr Gly Glu Tyr Gly Asp Met Val Glu Met Gly Ile Leu Asp Pro Thr 485 490 495
- Lys Val Thr Arg Met Ala Leu Gln Asn Ala Ala Ser Val Ala Ser Leu 500 505 510
- Met Leu Thr Thr Glu Cys Met Val Ala Asp Leu Pro Lys Lys Glu Glu 515 520 525
- Gly Val Gly Ala Gly Asp Met Gly Gly Met Gly Gly Met 530 535 540

Gly Gly Met Met Glx

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 541 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Ala Lys Thr Ile Ala Tyr Asp Glu Glu Ala Arg Arg Gly Leu Glu 1 5 10 15

Arg Gly Leu Asn Ala Leu Ala Asp Ala Val Lys Val Thr Leu Gly Pro

20 25 30

Lys Gly Arg Asn Val Val Leu Glu Lys Lys Trp Gly Ala Pro Thr Ile 4.0 Thr Asn Asp Gly Val Ser Ile Ala Lys Glu Ile Glu Leu Glu Asp Pro Tyr Glu Lys Ile Gly Ala Glu Leu Val Lys Glu Val Ala Lys Lys Thr 70 Asp Asp Val Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Gln Ala Leu Val Arg Glu Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro 105 Leu Gly Leu Lys Arg Gly Ile Glu Lys Ala Val Glu Lys Val Thr Glu 115 120 Thr Leu Leu Lys Ser Ala Lys Glu Val Glu Thr Lys Asp Gln Ile Ala 135 Ala Thr Ala Ala Ile Ser Ala Gly Asp Gln Ser Ile Gly Asp Leu Ile Ala Glu Ala Met Asp Lys Val Gly Asn Glu Gly Val Ile Thr Val Glu 165 170 Glu Ser Asn Thr Phe Gly Leu Gln Leu Glu Leu Thr Glu Gly Met Arg 185 Phe Asp Lys Gly Tyr Ile Ser Gly Tyr Phe Val Thr Asp Ala Glu Arg 195 Gln Glu Ala Val Leu Glu Asp Pro Phe Ile Leu Leu Val Ser Ser Lys 215 Val Ser Thr Val Lys Asp Leu Leu Pro Leu Leu Glu Lys Val Ile Gln 225 230 235 240 Ala Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly Glu Ala Leu Ser Thr Leu Val Val Asn Lys Ile Arg Gly Thr Phe Lys Ser Val Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met Leu Gln 275 280 Asp Met Ala Ile Leu Thr Gly Gly Gln Val Ile Ser Glu Glu Val Gly 295 Leu Ser Leu Glu Ser Ala Asp Ile Ser Leu Leu Gly Lys Ala Arg Lys 305 310 315 320 Val Val Thr Lys Asp Glu Thr Thr Ile Val Glu Gly Ala Gly Asp

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- Ser Asp Ala Ile Ala Gly Arg Val Ala Gln Ile Arg Thr Glu Ile Glu 340 345 350
- Asn Ser Asp Ser Asp Tyr Asp Arg Glu Lys Leu Gln Glu Arg Leu Ala 355 360 365
- Lys Leu Ala Gly Gly Val Ala Val Ile Lys Ala Gly Ala Ala Thr Glu 370 375 380
- Val Glu Leu Lys Glu Arg Lys His Arg Ile Glu Asp Ala Val Arg Asm 385 390 395 400
- Ala Lys Ala Ala Val Glu Glu Gly Ile Val Ala Gly Gly Gly Val Ala 405 410 415
- Leu Leu His Ala Ile Pro Ala Leu Asp Glu Leu Lys Pro Glu Gly Glu
 420 425 430
- Glu Ala Thr Gly Ala Asn Ile Val Arg Val Ala Leu Glu Arg Pro Leu 435 440 445
- Lys Gln Ile Ala Phe Asn Gly Gly Leu Glu Pro Gly Val Val Ala Glu 450 455 460
- Lys Val Arg Asn Ser Pro Ala Gly Thr Gly Leu Asn Ala Ala Thr Gly 465 470 475 480
- Glu Tyr Glu Asp Leu Leu Lys Ala Gly Ile Ala Asp Pro Val Lys Val
 485 490 495
- Thr Arg Ser Ala Leu Gln Asn Ala Ala Ser Ile Ala Gly Leu Phe Leu 500 505 510
- Thr Thr Glu Ala Val Val Ala Asp Lys Pro Glu Lys Ala Ala Ala Pro 515 520 525
- Ala Gly Asp Pro Thr Gly Gly Met Gly Gly Met Asp Phe 530 535 540

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 540 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Ala Lys Thr Ile Ala Tyr Asp Glu Glu Ala Arg Arg Gly Leu Glu 1 5 10 15

Arg Gly Leu Asn Ala Leu Ala Asp Ala Val Lys Val Thr Leu Gly Pro

20 25 30

Lys Gly Arg Asn Val Val Leu Glu Lys Lys Trp Gly Ala Pro Thr Ile 40 Thr Asn Asp Gly Val Ser Ile Ala Lys Glu Ile Glu Leu Glu Asp Pro Tyr Glu Lys Ile Gly Ala Glu Leu Val Lys Glu Val Ala Lys Lys Thr 75 Asp Asp Val Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Gln Ala Leu Val Arg Glu Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro 105 Leu Gly Leu Lys Arg Gly Ile Glu Lys Ala Val Glu Lys Val Thr Glu 115 120 Thr Leu Leu Lys Gly Ala Lys Glu Val Glu Thr Lys Glu Gln Ile Ala 135 Ala Thr Ala Ala Ile Ser Ala Gly Asp Gln Ser Ile Gly Asp Leu Ile 150 155 Ala Glu Ala Met Asp Lys Val Gly Asn Glu Gly Val Ile Thr Val Glu 165 170 Glu Ser Asn Thr Phe Gly Leu Gln Leu Glu Leu Thr Glu Gly Met Arg 185 Phe Asp Lys Gly Tyr Ile Ser Gly Tyr Phe Val Thr Asp Pro Glu Arg Gln Glu Ala Val Leu Glu Asp Pro Tyr Ile Leu Leu Val Ser Ser Lys 215 Val Ser Thr Val Lys Asp Leu Leu Pro Leu Leu Glu Lys Val Ile Gly 225 230 235 240 Ala Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly Glu Ala 250 Leu Ser Thr Leu Val Val Asn Lys Ile Arg Gly Thr Phe Lys Ser Val Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Lys Ala Met Leu Gln 275 280 285 Asp Met Ala Ile Leu Thr Gly Gly Gln Val Ile Ser Glu Glu Val Gly 295 Leu Thr Leu Glu Asn Ala Asp Leu Ser Leu Leu Gly Lys Ala Arg Lys 305 310 315 320 Val Val Thr Lys Asp Glu Thr Thr Ile Val Glu Gly Ala Gly Asp 325 330

- Thr Asp Ala Ile Ala Gly Arg Val Ala Gln Ile Arg Gln Glu Ile Glu 340 345 350
- Asn Ser Asp Ser Asp Tyr Asp Arg Glu Lys Leu Gln Glu Arg Leu Ala 355 360 365
- Lys Leu Ala Gly Gly Val Ala Val Ile Lys Ala Gly Ala Ala Thr Glu 370 375 380
- Val Glu Leu Lys Glu Arg Lys His Arg Ile Glu Asp Ala Val Arg Asn 385 390 395 400
- Ala Lys Ala Ala Val Glu Glu Gly Ile Val Ala Gly Gly Val Thr 405 410 415
- Leu Leu Gln Ala Ala Pro Thr Leu Asp Glu Leu Lys Leu Glu Gly Asp
 420 425 430
- Glu Ala Thr Gly Ala Asn Ile Val Lys Val Ala Leu Glu Ala Pro Leu 435 440 445
- Lys Gln Ile Ala Phe Asn Ser Gly Leu Glu Pro Gly Val Val Ala Glu 450 455 460
- Lys Val Arg Asn Leu Pro Ala Gly His Gly Leu Asn Ala Gln Thr Gly 465 470 475 480
- Val Tyr Glu Asp Leu Leu Ala Ala Gly Val Ala Asp Pro Val Lys Val
 485 490 495
- Thr Arg Ser Ala Leu Gln Asn Ala Ala Ser Ile Ala Gly Leu Phe Leu 500 505 510
- Thr Thr Glu Ala Val Val Ala Asp Lys Pro Glu Lys Glu Lys Ala Ser 515 520 525
- Val Pro Gly Gly Gly Asp Met Gly Gly Met Asp Phe 530 535 540
- (2) INFORMATION FOR SEQ ID NO:16:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 537 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
 - Met Ser Lys Leu Ile Glu Tyr Asp Glu Thr Ala Arg His Ala Met Glu 1 5 10 15
 - Val Gly Met Asn Lys Leu Ala Asp Thr Val Arg Val Thr Leu Gly Pro

20 25 30

Arg Gly Arg His Val Val Leu Ala Lys Ala Phe Gly Gly Pro Thr Ile 4.0 Thr Asn Asp Gly Val Thr Val Ala Arg Glu Ile Asp Leu Glu Asp Pro Phe Glu Asn Leu Gly Ala Gln Leu Val Lys Ser Val Ala Thr Lys Thr 70 75 Asn Asp Val Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Gln 90 Ala Leu Val Lys Gly Gly Leu Arg Met Val Ala Ala Gly Ala Asn Pro Val Ala Leu Gly Ala Gly Ile Ser Lys Ala Ala Asp Ala Val Ser Glu 120 Ala Leu Leu Ala Val Ala Thr Pro Val Ala Gly Lys Asp Ala Ile Thr 135 Gln Val Ala Thr Val Ser Ser Arg Asp Glu Gln Ile Gly Ala Leu Val Gly Glu Gly Met Asn Lys Val Gly Thr Asp Gly Val Val Ser Val Glu 170 Glu Ser Ser Thr Leu Asp Thr Glu Leu Glu Phe Thr Glu Gly Val Gly 185 Phe Asp Lys Gly Phe Leu Ser Ala Tyr Phe Val Thr Asp Phe Asp Ser 195 200 Gln Gln Ala Val Leu Asp Asp Pro Leu Val Leu Leu His Gln Glu Lys 215 Ile Ser Ser Leu Pro Glu Leu Leu Pro Met Leu Glu Lys Val Thr Glu 225 230 235 240 Ser Gly Lys Pro Leu Leu Ile Val Ala Glu Asp Leu Glu Gly Glu Ala 250 Leu Ala Thr Leu Val Val Asn Ser Ile Arg Lys Thr Leu Lys Ala Val 265 Ala Val Lys Ser Pro Phe Phe Gly Asp Arg Lys Ala Phe Leu Glu 275 280 Asp Leu Ala Ile Val Thr Gly Gly Gln Val Val Asn Pro Glu Thr Gly 295 Leu Val Leu Arg Glu Val Gly Thr Asp Val Leu Gly Ser Ala Arg Arg 305 310 315 320 Val Val Val Ser Lys Asp Asp Thr Ile Ile Val Asp Gly Gly Ser

330

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- Asn Asp Ala Val Ala Lys Arg Val Asn Gln Leu Arg Ala Glu Ile Glu 340 345 350
- Val Ser Asp Ser Glu Trp Asp Arg Glu Lys Leu Gln Glu Arg Val Ala 355 360 365
- Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Val Thr Glu 370 375 380
- Thr Ala Leu Lys Lys Arg Lys Glu Ser Val Glu Asp Ala Val Ala Ala 385 390 395 400
- Ala Lys Ala Ser Ile Glu Glu Gly Ile Ile Ala Gly Gly Gly Ser Ala 405 410 415
- Leu Val Gln Cys Gly Ala Ala Leu Lys Gln Leu Arg Thr Ser Leu Thr 420 425 430
- Gly Asp Glu Ala Leu Gly Ile Asp Val Phe Phe Glu Ala Leu Lys Ala 435 440 445
- Pro Leu Tyr Trp Ile Ala Thr Asn Ala Gly Leu Asp Gly Ala Val Val 450 455 460
- Val Asp Lys Val Ser Gly Leu Pro Ala Gly His Gly Leu Asn Ala Ser 465 470 475 480
- Thr Leu Gly Tyr Gly Asp Leu Val Ala Asp Gly Val Val Asp Pro Val
 485 490 495
- Lys Val Thr Arg Ser Ala Val Leu Asn Ala Ala Ser Val Ala Arg Met 500 505 510
- Met Leu Thr Thr Glu Thr Ala Val Val Asp Lys Pro Ala Lys Thr Glu 515 520 525
- Glu His Asp His His Gly His Ala His

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 541 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Ala Lys Thr Ile Ala Tyr Asp Glu Glu Ala Arg Arg Gly Leu Glu 1 5 10 15

Arg Gly Leu Asn Ser Leu Ala Asp Ala Val Lys Val Thr Leu Gly Pro

20 25 30

Lys Gly Arg Asn Val Val Leu Glu Lys Lys Trp Gly Ala Pro Thr Ile 40 Thr Asn Asp Gly Val Ser Ile Ala Lys Glu Ile Glu Leu Glu Asp Pro Tyr Glu Lys Ile Gly Ala Glu Leu Val Lys Glu Val Ala Lys Lys Thr Asp Asp Val Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Gln Ala Leu Val Lys Glu Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro Leu Gly Leu Lys Arg Gly Ile Glu Lys Ala Val Asp Lys Val Thr Glu 120 Thr Leu Leu Lys Asp Ala Lys Glu Val Glu Thr Lys Glu Gln Ile Ala 135 Ala Thr Ala Ala Ile Ser Ala Gly Asp Gln Ser Ile Gly Asp Leu Ile Ala Glu Ala Met Asp Lys Val Gly Met Glu Gly Val Ile Thr Val Glu 170 Glu Ser Asn Thr Phe Gly Leu Gln Leu Glu Leu Thr Glu Gly Met Arg 185 Phe Asp Lys Gly Tyr Ile Ser Gly Tyr Phe Val Thr Asp Ala Glu Arg 195 Gln Glu Ala Val Leu Glu Pro Tyr Ile Leu Leu Val Ser Ser Lys Val Ser Thr Val Lys Asp Leu Leu Pro Leu Leu Glu Lys Val Ile Gln 225 230 235 240 Ala Gly Lys Ser Leu Leu Ile Ile Ala Glu Asp Val Glu Gly Glu Ala Leu Ser Thr Leu Val Val Asn Lys Ile Arg Gly Thr Phe Lys Ser Val 265 Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met Leu Gln 275 280 Asp Met Ala Ile Leu Thr Gly Ala Gln Val Ile Ser Glu Glu Val Gly 295 Leu Thr Leu Glu Asn Thr Asp Leu Ser Leu Leu Gly Lys Ala Arg Lys 305 310 315 320 Val Val Met Thr Lys Asp Glu Thr Thr Ile Val Glu Gly Ala Gly Asp 325 330 335

- Thr Asp Ala Ile Ala Gly Arg Val Ala Gln Ile Arg Thr Glu Ile Glu
 340 345 350
- Asn Ser Asp Ser Asp Tyr Asp Arg Glu Lys Leu Gln Glu Arg Leu Ala 355 360 365
- Lys Leu Ala Gly Gly Val Ala Val Ile Lys Ala Gly Ala Ala Thr Glu 370 375 380
- Val Glu Leu Lys Glu Arg Lys His Arg Ile Glu Asp Ala Val Arg Asn 385 390 395 400
- Ala Lys Ala Ala Val Glu Glu Gly Ile Val Ala Gly Gly Val Thr 405 410 415
- Leu Leu Gln Ala Ala Pro Ala Leu Asp Lys Leu Lys Leu Thr Gly Asp
 420 425 430
- Glu Ala Thr Gly Ala Asn Ile Val Lys Val Ala Leu Glu Ala Pro Leu 435 440 445
- Lys Gln Ile Ala Phe Asn Ser Gly Met Glu Pro Gly Val Val Ala Glu 450 460
- Lys Val Arg Asn Leu Ser Val Gly His Gly Leu Asn Ala Ala Thr Gly 465 470 475 480
- Glu Tyr Glu Asp Leu Leu Lys Ala Gly Val Ala Asp Pro Val Lys Val
 485 490 495
- Thr Arg Ser Ala Leu Gln Asn Ala Ala Ser Ile Ala Gly Leu Phe Leu 500 505 510
- Thr Thr Glu Ala Val Val Ala Asp Lys Pro Glu Lys Thr Ala Ala Pro 515 520 525
- Ala Ser Asp Pro Thr Gly Gly Met Gly Gly Met Asp Phe 530 535 540

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 539 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Ser Lys Leu Ile Glu Tyr Asp Glu Thr Ala Arg Arg Ala Met Glu 1 5 10 15

Val Gly Met Asp Lys Leu Ala Asp Thr Val Arg Val Thr Leu Gly Pro

Arg Gly Arg His Val Val Leu Ala Lys Ala Phe Gly Gly Pro Thr Val 4.0 Thr Asn Asp Gly Val Thr Val Ala Arg Glu Ile Glu Leu Glu Asp Pro Phe Glu Asp Leu Gly Ala Gln Leu Val Lys Ser Val Ala Thr Lys Thr Asn Asp Val Ala Gly Asp Gly Thr Thr Thr Ala Thr Ile Leu Ala Gln Ala Leu Ile Lys Gly Gly Leu Arg Leu Val Ala Ala Gly Val Asn Pro Ile Ala Leu Gly Val Gly Ile Gly Lys Ala Ala Asp Ala Val Ser Glu Ala Leu Leu Ala Ser Ala Thr Pro Val Ser Gly Lys Thr Gly Ile Ala Gln Val Ala Thr Val Ser Ser Arg Asp Glu Gln Ile Gly Asp Leu Val Gly Glu Ala Met Ser Lys Val Gly His Asp Gly Val Val Ser Val Glu Glu Ser Ser Thr Leu Gly Thr Glu Leu Glu Phe Thr Glu Gly Ile Gly Phe Asp Lys Gly Phe Leu Ser Ala Tyr Phe Val Thr Asp Phe Asp Asn Gln Gln Ala Val Leu Glu Asp Ala Leu Ile Leu Leu His Gln Asp Lys Ile Ser Ser Leu Pro Asp Leu Leu Pro Leu Leu Glu Lys Val Ala Gly Thr Gly Lys Pro Leu Leu Ile Val Ala Glu Asp Val Glu Gly Glu Ala Leu Ala Thr Leu Val Val Asn Ala Ile Arg Lys Thr Leu Lys Ala Val Ala Val Lys Gly Pro Tyr Phe Gly Asp Arg Arg Lys Ala Phe Leu Glu Asp Leu Ala Val Val Thr Gly Gly Gln Val Val Asn Pro Asp Ala Gly Met Val Leu Arg Glu Val Gly Leu Glu Val Leu Gly Ser Ala Arg Arg Val Val Ser Lys Asp Asp Thr Val Ile Val Asp Gly Gly Thr

- Ala Glu Ala Val Ala Asn Arg Ala Lys His Leu Arg Ala Glu Ile Asp 340 345 350
- Lys Ser Asp Ser Asp Trp Asp Arg Glu Lys Leu Gly Glu Arg Leu Ala 355 360 365
- Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala Thr Glu 370 380
- Thr Ala Leu Lys Glu Arg Lys Glu Ser Val Glu Asp Ala Val Ala Ala 385 390 395 400
- Ala Lys Ala Ala Val Glu Glu Gly Ile Val Pro Gly Gly Gly Ala Ser 405 410 415
- Leu Ile His Gln Ala Arg Lys Ala Leu Thr Glu Leu Arg Ala Ser Leu 420 425 430
- Thr Gly Asp Glu Val Leu Gly Val Asp Val Phe Ser Glu Ala Leu Ala 435 440 445
- Ala Pro Leu Phe Trp Ile Ala Ala Asn Ala Gly Leu Asp Gly Ser Val 450 455 460
- Val Val Lys Lys Val Ser Glu Leu Pro Ala Gly His Gly Leu Asn Val 465 470 475 480
- Asn Thr Leu Ser Tyr Gly Asp Leu Ala Ala Asp Gly Val Ile Asp Pro 485 490 495
- Val Lys Val Thr Arg Ser Ala Val Leu Asn Ala Ser Ser Val Ala Arg 500 505 510
- Met Val Leu Thr Thr Glu Thr Val Val Val Asp Lys Pro Ala Lys Ala 515 520 525
- Glu Asp His Asp His His His Gly His Ala His 530 535

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 545 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Ala Ala Lys Asp Val Gln Phe Gly Asn Glu Val Arg Gln Lys Met 1 $$ 5 $$ 10 $$ 15

Val Asn Gly Val Asn Ile Leu Ala Asn Ala Val Arg Val Thr Leu Gly

Pro Lys Gly Arg Asn Val Val Val Asp Arg Ala Phe Gly Gly Pro His 35 40 45

Ile Thr Lys Asp Gly Val Thr Val Ala Lys Glu Ile Glu Leu Lys Asp 50 55 60

Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Lys 65 70 75 80

Thr Asn Asp Val Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala 85 90 95

Gln Ser Ile Val Ala Glu Gly Met Lys Tyr Val Thr Ala Gly Met Asn 100 105 110

Pro Thr Asp Leu Lys Arg Gly Ile Asp Lys Ala Val Ala Ala Leu Val 115 120 125

Glu Glu Leu Lys Asn Ile Ala Lys Pro Cys Asp Thr Ser Lys Glu Ile 130 135 140

Ala Gln Val Gly Ser Ile Ser Ala Asn Ser Asp Glu Gln Val Gly Ala 145 150 155 160

Ile Ile Ala Glu Ala Met Glu Lys Val Gly Lys Glu Gly Val Ile Thr
165 170 175

Val Glu Asp Gly Lys Ser Leu Glu Asn Glu Leu Asp Val Val Glu Gly
180 185 190

Met Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Ile Asn Asp Ala 195 200 205

Glu Lys Gln Ile Ala Gly Leu Asp Asn Pro Phe Val Leu Leu Phe Asp 210 215 220

Lys Lys Ile Ser Asn Ile Arg Asp Leu Leu Pro Val Leu Glu Gln Val 225 230 235 240

Ala Lys Ala Ser Arg Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly
245 250 255

Glu Ala Leu Ala Thr Leu Val Val Asn Asn Ile Arg Gly Ile Leu Lys
260 265 270

Thr Val Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Lys Ala Met 275 280 285

Leu Gln Asp Ile Ala Ile Leu Thr Gly Gly Thr Val Ile Ser Glu Glu 290 295 300

Val Gly Leu Ser Leu Glu Lys Ala Thr Leu Asp Asp Leu Gly Gln Ala 305 310 315 320

Lys Arg Ile Glu Ile Gly Lys Glu Asn Thr Thr Ile Ile Asp Gly Phe 325 330 335

Gly Asp Ala Ala Gln Ile Glu Ala Arg Val Ala Glu Ile Arg Gln Gln 340 345 350

Ile Glu Thr Ala Thr Ser Asp Tyr Asp Lys Glu Lys Leu Gln Glu Arg 355 360 365

Val Ala Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala 370 375 380

Thr Glu Val Glu Met Lys Glu Lys Lys Asp Arg Val Glu Asp Ala Leu 385 390 395 400

His Ala Thr Arg Ala Ala Val Glu Glu Gly Val Val Ala Gly Gly Gly 405 410 415

Val Ala Leu Leu Arg Ala Arg Ala Leu Glu Asn Leu His Thr Gly
420 425 430

Asn Ala Asp Gln Asp Ala Gly Val Gln Ile Val Leu Arg Ala Val Glu 435 440 445

Ser Pro Leu Arg Gln Ile Val Ala Asn Ala Gly Gly Glu Pro Ser Val 450 455 460

Val Val Asn Lys Val Leu Glu Gly Lys Gly Asn Tyr Gly Tyr Asn Ala 465 470 475 480

Gly Ser Gly Glu Tyr Gly Asp Met Ile Glu Met Gly Val Leu Asp Pro 485 490 495

Ala Lys Val Thr Arg Ser Ala Leu Gln His Ala Ala Ser Ile Ala Gly 500 505 510

Leu Met Leu Thr Thr Asp Cys Met Ile Ala Glu Ile Pro Glu Glu Lys 515 520 525

Pro Ala Met Pro Asp Met Gly Gly Met Gly Gly Met Gly Gly Met Met 530 535 540

Glx 545

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 539 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Val Lys Gln Leu Lys Phe Ser Glu Asp Ala Arg Gln Ala Met Leu

Arg Gly Val Asp Gln Leu Ala Asn Ala Val Lys Val Thr Ile Gly Pro 20 25 Lys Gly Arg Asn Val Val Leu Asp Lys Glu Phe Thr Ala Pro Leu Ile Thr Asn Asp Gly Val Thr Ile Ala Lys Glu Ile Glu Leu Glu Asp Pro Tyr Glu Asn Met Gly Ala Lys Leu Val Gln Glu Val Ala Asn Lys Thr Asn Glu Ile Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Gln 90 Ala Met Ile Gln Glu Gly Leu Lys Asn Val Thr Ser Gly Ala Asn Pro 100 Val Gly Leu Arg Gln Gly Ile Asp Lys Ala Val Lys Val Ala Val Glu 120 Ala Leu His Glu Asn Ser Gln Lys Val Glu Asn Lys Asn Glu Ile Ala 130 135 140 Gln Val Gly Ala Ile Ser Ala Ala Asp Glu Glu Ile Gly Arg Tyr Ile 150 155 Ser Glu Ala Thr Glu Lys Val Gly Asn Asp Gly Val Ile Thr Ile Ile 165 170 Thr Ile Glu Glu Ser Asn Arg Leu Asn Thr Glu Leu Glu Leu Gly Met 180 Gln Phe Asp Arg Gly Tyr Gln Ser Pro Tyr Met Val Thr Asp Ser Asp 200 Lys Met Val Ala Glu Leu Glu Arg Pro Tyr Ile Leu Val Thr Asp Lys 215 220 210 Lys Ile Ser Ser Phe Gln Asp Ile Leu Pro Leu Leu Glu Gln Val Val 225 . 230 235 Gln Ser Asn Arg Pro Ile Leu Ile Val Ala Asp Glu Val Glu Gly Asp 250 Ala Leu Thr Asn Ile Val Leu Asn Arg Met Arg Gly Thr Phe Thr Ala 260 265 270

Val Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met Leu 275 280 285

Glu Asp Leu Ala Ile Leu Thr Gly Ala Gln Val Ile Thr Asp Asp Leu

Gly Leu Asp Leu Lys Asp Ala Ser Ile Asp Met Leu Gly Thr Ala Ser

300

315

295

310

290

- Lys Val Glu Val Thr Lys Asp Asn Thr Thr Val Val Asp Gly Asp Gly 325 330 335
- Asp Glu Asn Ser Ile Asp Ala Arg Val Ser Gln Leu Lys Ser Gln Ile 340 345 350
- Glu Glu Thr Glu Ser Asp Phe Asp Arg Glu Lys Leu Gln Glu Arg Leu 355 360 365
- Ala Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala Ser 370 380
- Glu Thr Glu Leu Lys Glu Arg Lys Leu Arg Ile Glu Asp Ala Leu Asn 385 390 395 400
- Ser Thr Arg Ala Ala Val Glu Glu Gly Ile Val Ala Gly Gly Gly Thr 405 410 415
- Ala Leu Val Asn Val Tyr Gln Lys Val Ser Glu Asn Glu Ala Glu Gly 420 425 430
- Asp Ile Glu Thr Gly Val Asn Ile Val Leu Lys Ala Leu Thr Ala Pro 435 440 445
- Val Arg Gln Ile Ala Glu Asn Ala Gly Leu Glu Gly Ser Val Ile Val 450 455 460
- Glu Arg Leu Lys Asn Ala Glu Pro Gly Val Gly Phe Asn Gly Ala Thr 465 470 475 480
- Asn Glu Trp Val Asn Met Leu Arg Arg Gly Ile Val Asp Pro Thr Lys 485 490 495
- Val Thr Arg Ser Ala Leu Gln His Ala Ala Ser Val Ala Ala Met Phe 500 505 510
- Leu Thr Thr Glu Ala Val Val Ala Ser Ile Pro Glu Lys Asn Asn Asp 515 520 525
- Gln Pro Asn Met Gly Gly Met Pro Gly Met Met 530 535

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 541 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Ala Lys Ser Ile Ile Tyr Asn Asp Glu Ala Arg Arg Ala Leu Glu

Arg Gly Met Asp Ile Leu Ala Glu Ala Val Ala Val Thr Leu Gly Pro Lys Gly Arg Asn Val Val Leu Glu Lys Lys Phe Gly Ser Pro Gln Ile Ile Asn Asp Gly Ile Thr Ile Ala Lys Glu Ile Glu Leu Glu Asp His Val Glu Asn Thr Gly Val Ser Leu Ile Arg Gln Ala Ala Ser Lys Thr Asn Asp Val Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala His Ala Ile Val Lys Glu Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro Ile Ser Leu Lys Arg Gly Ile Asp Lys Ala Thr Asp Phe Leu Val Ala Arg Ile Lys Glu His Ala Gln Pro Val Gly Asp Ser Lys Ala Ile Ala Gln Val Gly Ala Ile Ser Ala Gly Asn Asp Glu Glu Val Gly Gln Met Ile Ala Asn Ala Met Asp Lys Val Gly Gln Glu Gly Val Ile Ser Leu Glu Glu Gly Lys Ser Met Thr Thr Glu Leu Glu Ile Thr Glu Gly Met Arg Phe Asp Lys Gly Tyr Ile Ser Pro Tyr Phe Val Thr Asp Ala Glu Arg Met Glu Ala Val Leu Glu Asp Pro Arg Ile Leu Ile Thr Asp Lys Lys Ile Asn Leu Val Gln Asp Leu Val Pro Ile Leu Glu Gln Val Ala Arg Gln Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Ile Glu Lys Glu Ala Leu Ala Thr Leu Val Val Asn Arg Leu Arg Gly Val Leu Asn Val Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Lys Gln Met Leu Glu Asp Ile Ala Thr Leu Thr Gly Gly Gln Val Ile Ser Glu Asp Ala Gly Leu Lys Leu Glu Ser Ala Thr Val Asp Ser Leu Gly Ser Ala Arg

- Arg Ile Asn Ile Thr Lys Asp Asn Thr Thr Ile Val Ala Glu Gly Asn 325 330 335
- Glu Ala Ala Val Lys Ser Arg Cys Glu Gln Ile Arg Arg Gln Ile Glu 340 345 350
- Glu Thr Asp Ser Ser Tyr Asp Lys Glu Lys Leu Gln Glu Arg Leu Ala 355 360 365
- Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala Thr Glu 370 380
- Thr Glu Met Lys Asp Arg Lys Leu Arg Leu Glu Asp Ala Ile Asn Ala 385 390 395 400
- Thr Lys Ala Ala Val Glu Glu Gly Ile Val Pro Gly Gly Gly Thr Thr
 405 410 415
- Leu Ala His Leu Ala Pro Gln Leu Glu Asp Trp Ala Thr Gly Asn Leu 420 425 430
- Lys Asp Glu Glu Leu Thr Gly Ala Leu Ile Val Ala Arg Ala Leu Pro 435 440 445
- Ala Pro Leu Lys Arg Ile Ala Glu Asn Ala Gly Gln Asn Gly Ala Val 450 455 460
- Ile Ser Glu Arg Val Lys Glu Lys Glu Phe Asn Val Gly Tyr Asn Ala 465 470 475 480
- Ala Ser Leu Glu Tyr Val Asp Met Leu Ala Ala Gly Ile Val Asp Pro 485 490 495
- Ala Lys Val Thr Arg Ser Ala Leu Gln Asn Ala Ala Ser Ile Ala Gly 500 505 510
- Met Val Leu Thr Thr Glu Cys Ile Val Val Asp Lys Pro Glu Lys Glu 515 520 525
- Lys Ala Pro Ala Gly Ala Pro Gly Gly Asp Phe Asp Tyr 530 535 540
- (2) INFORMATION FOR SEQ ID NO:22:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 552 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Ser Lys Leu Ile Ser Phe Lys Asp Glu Ser Arg Arg Ser Leu Glu

Ala Gly Ile Asn Ala Leu Ala Asp Ala Val Arg Ile Thr Leu Gly Pro 2.0 25 Lys Gly Arg Asn Val Leu Leu Glu Lys Gln Tyr Gly Ala Pro Gln Ile Val Asn Asp Gly Ile Thr Val Ala Lys Glu Ile Glu Leu Ser Asn Pro Glu Glu Asn Ala Gly Ala Lys Leu Ile Gln Glu Val Ala Ser Lys Thr Lys Glu Ile Ala Gly Asp Gly Thr Thr Thr Ala Thr Ile Ile Ala Gln 90 Ala Leu Val Arg Glu Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro 100 105 Val Ala Leu Arg Arg Gly Ile Glu Lys Val Thr Thr Phe Leu Val Gln 120 Glu Ile Glu Ala Val Ala Lys Pro Val Glu Gly Ser Ala Ile Ala Gln 135 140 Val Ala Thr Val Ser Ser Gly Asn Asp Pro Glu Val Gly Ala Met Ile 150 155 Ala Asp Ala Met Asp Lys Val Thr Lys Asp Gly Val Ile Thr Val Glu 165 170 Glu Ser Lys Ser Leu Asn Thr Glu Leu Glu Val Val Glu Gly Met Gln 180 Ile Asp Arg Gly Tyr Ile Ser Pro Tyr Phe Ile Thr Asp Ser Asp Arg 200 Gln Leu Val Glu Phe Asp Asn Pro Leu Ile Leu Ile Thr Asp Lys Lys 210 220 215 Ile Ser Ala Ile Ala Glu Leu Val Pro Val Leu Glu Ala Val Ala Arg 225 230 Ala Gly Arg Pro Leu Leu Ile Ile Ala Glu Asp Ile Glu Gly Glu Ala 250 Leu Ala Thr Leu Val Val Asn Lys Ala Arg Gly Val Leu Asn Val Ala 260 265 270 Ala Ile Lys Ala Pro Ala Phe Gly Asp Arg Lys Ala Val Leu Gln 280 Asp Ile Ala Ile Leu Thr Gly Gly Ser Val Ile Ser Glu Asp Ile Gly 290 295 300 Leu Ser Leu Asp Thr Val Ser Leu Asp Gln Leu Gly Gln Ala Val Lys

310

Ala Thr Leu Glu Lys Asp Asn Thr Ile Leu Val Ala Gly Ala Asp Lys 325 330 335

Arg Ala Ser Ala Gly Val Lys Glu Arg Ile Glu Gln Leu Arg Lys Glu 340 345 350

Tyr Ala Ala Ser Asp Ser Asp Tyr Asp Lys Glu Lys Ile Gln Glu Arg 355 360 365

Ile Ala Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala 370 375 380

Thr Glu Thr Glu Leu Lys Asp Arg Lys Leu Arg Ile Glu Asp Ala Leu 385 390 395 400

Asn Ala Thr Lys Ala Ala Val Glu Glu Gly Ile Val Pro Gly Gly 405 410 415

Thr Thr Leu Ile Arg Leu Ala Gly Lys Ile Glu Ser Phe Lys Ala Gln
420 425 430

Leu Ser Asn Asp Glu Glu Arg Val Ala Ala Asp Ile Ile Ala Lys Ala 435 440 445

Leu Glu Ala Pro Leu His Gln Leu Ala Ser Asn Ala Gly Val Glu Gly 450 455 460

Ser Val Ile Val Glu Lys Val Lys Glu Ala Thr Gly Asn Gln Gly Tyr 465 470 475 480

Asn Val Ile Thr Gly Lys Ile Glu Asp Leu Ile Ala Ala Gly Ile Ile 485 490 495

Asp Pro Ala Lys Val Val Arg Ser Ala Leu Gln Asn Ala Ala Ser Ile 500 505 510

Ala Gly Met Val Leu Thr Thr Glu Ala Leu Val Val Glu Lys Pro Glu 515 520 525

Pro Ala Ala Pro Ala Met Pro Asp Met Gly Gly Met Gly Gly Met Gly 530 540

Gly Met Gly Gly Met Gly Met Met 545 550

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 539 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

- Met Ala Lys Thr Ile Ala Phe Asp Lys Lys Ala Arg Arg Gly Leu Glu 1 10 15
- Arg Gly Leu Asn Ala Leu Ala Asp Ala Val Lys Val Thr Leu Gly Pro 20 25 30
- Lys Gly Arg Asn Val Val Leu Glu Lys Lys Trp Gly Ala Pro Thr Ile $35 \hspace{1cm} 40 \hspace{1cm} 45$
- Thr Asn Asp Gly Val Ser Ile Ala Lys Glu Ile Glu Leu Glu Asp Pro 50 55 60
- Tyr Glu Lys Ile Gly Ala Glu Leu Val Lys Glu Val Ala Lys Lys Thr 65 70 75 80
- Asp Asp Val Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Gln
 85 90 95
- Ala Leu Val Arg Glu Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro 100 105 110
- Leu Gly Leu Lys Arg Gly Ile Glu Lys Ala Val Glu Ala Val Thr Glu 115 120 125
- His Leu Leu Lys Ala Ala Lys Glu Val Glu Thr Lys Asp Gln Ile Ala 130 135 140
- Ala Thr Ala Gly Ile Ser Ala Gly Asp Pro Ala Ile Gly Glu Leu Ile 145 150 155 160
- Ala Glu Ala Met Asp Lys Val Gly Lys Glu Gly Val Ile Thr Val Glu 165 170 175
- Glu Ser Asn Thr Phe Gly Leu Gln Leu Glu Leu Thr Glu Gly Met Arg 180 185 190
- Phe Asp Lys Gly Phe Ile Ser Gly Tyr Phe Ala Thr Asp Ala Glu Arg 195 200 205
- Gln Glu Ala Val Leu Glu Asp Pro Tyr Val Leu Leu Val Ser Gly Lys 210 215 220
- Ile Ser Thr Val Lys Asp Leu Leu Pro Leu Leu Glu Lys Val Ile Gln 225 230 235 240
- Ser Gly Lys Pro Leu Ala Ile Ile Ala Glu Asp Val Glu Gly Glu Ala 245 250 255
- Leu Val Thr Leu Ile Val Asn Lys Ile Arg Gly Thr Phe Lys Ser Val 260 265 270
- Ala Ile Lys Ala Pro Gly Phe Gly Asp Arg Lys Ala Met Leu Gln 275 280 285
- Asp Met Ala Ile Leu Thr Gly Gly Gln Val Ile Ser Glu Glu Ile Gly 290 295 300

Leu Ser Leu Asp Thr Ala Gly Leu Glu Val Leu Gly Gln Ala Arg Gln 310 315 Val Val Val Thr Lys Asp Glu Thr Thr Ile Val Asp Gly Ala Gly Ser 330 Lys Glu Gln Ile Ala Gly Arg Val Ser Gln Ile Arg Ala Glu Ile Glu 345 Asn Ser Asp Ser Asp Tyr Asp Arg Glu Lys Leu Gln Glu Arg Leu Ala 355 360 Lys Leu Ala Gly Gly Val Ala Val Ile Lys Ala Gly Ala Ala Thr Glu 370 375 380 Asp Leu Lys Glu Arg Lys His Arg Ile Glu Asp Ala Val Arg Asn Ala 390 395 Lys Ala Ala Val Glu Glu Gly Ile Val Ala Gly Gly Ser Ser Leu Ala Gln Ser Gly Thr Val Phe Asp Ser Xaa Ala Leu Glu Gly Asp Glu 420 425 Ala Thr Gly Ala Asn Ile Val Lys Val Ala Leu Asp Ala Pro Val Lys 435 440 Gln Ile Ala Val Asn Ala Gly Leu Glu Pro Gly Val Val Ala Glu Lys 455 Val Arg Asn Ser Pro Ala Gly Thr Gly Leu Asn Ala Ala Thr Gly Val 470 475 Tyr Glu Asp Leu Leu Ala Ala Gly Ile Asn Asp Pro Val Lys Val Thr 485 490 Arg Ser Ala Leu Gln Asn Ala Ala Ser Ile Ala Ala Leu Phe Leu Thr 505

Thr Glu Ala Val Val Ala Asp Lys Pro Glu Lys Ala Gly Ala Pro Val 515 520 525

Asp Pro Thr Gly Gly Met Gly Gly Met Asp Phe 530 535

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 582 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:
- Met Val Ser Phe Leu Ser Ser Ser Val Ser Arg Leu Pro Leu Arg Ile 1 5 10 15
- Ala Gly Arg Arg Ile Pro Gly Arg Phe Ala Val Pro Gln Val Arg Thr 20 25 30
- Tyr Ala Lys Asp Leu Lys Phe Gly Val Asp Ala Arg Ala Ser Leu Leu 35 40 45
- Thr Gly Val Asp Thr Leu Ala Arg Ala Val Ser Val Thr Leu Gly Pro
 50 55 60
- Lys Gly Arg Asn Val Leu Ile Asp Gln Pro Phe Gly Ser Pro Lys Ile
 65 70 75 80
- Thr Lys Asp Gly Val Thr Val Ala Arg Ser Val Ser Leu Lys Asp Lys 85 90 95
- Phe Glu Asn Leu Gly Ala Arg Leu Val Gln Asp Val Ala Ser Lys Thr 100 105 110
- Asn Glu Val Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Thr Arg 115 120 125
- Ala Ile Phe Ser Glu Thr Val Arg Asn Val Ala Ala Gly Cys Asn Pro 130 135 140
- Met Asp Leu Arg Arg Gly Ile Gln Leu Ala Val Asp Asn Val Val Glu
 145 150 155, 160
- Phe Leu Gln Ala Asn Lys Arg Asp Ile Thr Thr Ser Glu Glu Ile Ser 165 170 175
- Gln Val Ala Thr Ile Ser Ala Asn Gly Asp Thr His Ile Gly Glu Leu 180 185 190
- Leu Ala Lys Ala Met Glu Arg Val Gly Lys Glu Gly Val Ile Thr Val
 195 200 205
- Lys Glu Gly Arg Thr Ile Ser Asp Glu Leu Glu Val Thr Glu Gly Met 210 215 220
- Lys Phe Asp Arg Gly Tyr Ile Ser Pro Tyr Phe Ile Thr Asp Val Lys 225 230 235 240
- Ser Gln Lys Val Glu Phe Glu Asn Pro Leu Ile Leu Leu Ser Glu Lys 245 250 255
- Lys Val Ser Ala Val Gln Asp Ile Leu Pro Ser Leu Glu Leu Ala Ala 260 265 270
- Gln Gln Arg Arg Pro Leu Val Ile Ile Ala Glu Asp Val Asp Gly Glu 275 280 285
- Ala Leu Ala Ala Cys Ile Leu Asn Lys Leu Arg Gly Gln Leu Gln Val 290 295 300

Val Ala Ile Lys Ala Pro Gly Phe Gly Asp Asn Arg Arg Asn Met Leu 310 315 Gly Asp Leu Ala Val Leu Thr Asp Ser Ala Val Phe Asn Asp Glu Ile 325 330 Asp Val Ser Ile Glu Lys Ala Gln Pro His His Leu Gly Ser Cys Gly 345 Ser Val Thr Val Thr Lys Glu Asp Thr Ile Ile Met Lys Gly Ala Gly 355 360 Asp His Val Lys Val Asn Asp Arg Cys Glu Gln Ile Arg Gly Val Met 375 Ala Asp Pro Asn Leu Thr Glu Ser Glu Lys Glu Lys Leu Gln Glu Arq 390 395 Leu Ala Lys Leu Ser Gly Gly Ile Ala Val Ile Lys Val Gly Ala Ser 405 Ser Glu Val Glu Val Asn Glu Lys Lys Asp Arg Ile Val Asp Ala Leu 420 425 Asn Ala Val Lys Ala Ala Val Ser Glu Gly Val Leu Pro Gly Ala Gly Thr Ser Phe Val Lys Ala Ser Leu Arg Leu Gly Asp Ile Pro Thr Asn 450 455 460 Asn Phe Asp Gln Lys Leu Gly Val Glu Ile Val Arg Lys Ala Ile Thr 465 470 475 Arg Pro Ala Gln Thr Ile Leu Glu Asn Ala Gly Leu Glu Gly Asn Leu 485 Ile Val Gly Lys Leu Lys Glu Leu Tyr Gly Lys Glu Phe Asn Ile Gly 505 Tyr Asp Ile Ala Lys Asp Arg Phe Val Asp Leu Asn Glu Ile Gly Val 515 520 525 Leu Asp Pro Leu Lys Val Val Arg Thr Gly Leu Val Isp Ala Ser Gly 530 Val Ala Ser Leu Met Gly Thr Thr Glu Cys Ala Ile Val Asp Ala Pro 550 555 Glu Glu Ser Lys Ala Pro Ala Gly Pro Pro Gly Met Gly Met Gly 565 570 Gly Met Pro Gly Met Met

(2) INFORMATION FOR SEQ ID NO:25:

⁽i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

- Met Leu Arg Ser Ser Val Val Arg Ser Arg Ala Thr Leu Arg Pro Leu 1 5 10 15
- Leu Arg Arg Ala Tyr Ser Ser His Lys Glu Leu Lys Phe Gly Val Glu
 20 25 30
- Gly Arg Ala Ser Leu Leu Lys Gly Val Glu Thr Leu Ala Glu Ala Val 35 40 45
- Ala Ala Thr Leu Gly Pro Lys Gly Arg Asn Val Leu Ile Glu Gln Pro 50 55 60
- Phe Gly Pro Pro Lys Ile Thr Lys Asp Gly Val Thr Val Ala Lys Ser 65 70 75 80
- Ile Val Leu Lys Asp Lys Phe Glu Asn Met Gly Ala Lys Leu Gln 85 90 95
- Glu Val Ala Ser Lys Thr Asn Glu Ala Ala Gly Asp Gly Thr Thr Ser 100 105 110
- Ala Thr Val Leu Gly Arg Ala Ile Phe Thr Glu Ser Val Lys Asn Val 115 120 125
- Ala Ala Gly Cys Asn Pro Met Asp Leu Arg Arg Gly Ser Gln Val Ala 130 135 140
- Val Glu Lys Val Ile Glu Phe Leu Ser Ala Asn Lys Lys Glu Ile Thr 145 150 155 160
- Thr Ser Glu Glu Ile Ala Gln Val Ala Thr Ile Ser Ala Asn Gly Asp 165 170 175
- Ser His Val Gly Lys Leu Leu Ala Ser Ala Met Glu Lys Val Gly Lys 180 185 190
- Glu Gly Val Ile Thr Ile Arg Glu Gly Arg Thr Leu Glu Asp Glu Leu 195 200 205
- Glu Val Thr Glu Gly Met Arg Phe Asp Arg Gly Phe Ile Ser Pro Tyr 210 215 220
- Phe Ile Thr Asp Pro Lys Ser Ser Lys Val Glu Phe Glu Lys Pro Leu 225 230 235 240
- Leu Leu Ser Glu Lys Lys Ile Ser Ser Ile Gln Asp Ile Leu Pro 245 250 255

- Ala Leu Glu Ile Ser Asn Gln Ser Arg Arg Pro Leu Leu Ile Ile Ala 260 265 270
- Glu Asp Val Asp Gly Glu Ala Leu Ala Ala Cys Ile Leu Asn Lys Leu 275 280 285
- Arg Gly Gln Val Lys Val Cys Ala Val Lys Ala Pro Gly Phe Gly Asp 290 295 300
- Asn Arg Lys Asn Thr Ile Gly Asp Ile Ala Val Leu Thr Gly Gly Thr 305 310 315 320
- Val Phe Thr Glu Glu Leu Asp Leu Lys Pro Glu Gln Cys Thr Ile Glu 325 330 335
- Asn Leu Gly Ser Cys Asp Ser Ile Thr Val Thr Lys Glu Asp Thr Val 340 345 350
- Ile Leu Asn Gly Ser Gly Pro Lys Glu Ala Ile Gln Glu Arg Ile Glu 355 360 365
- Gln Ile Lys Gly Ser Ile Asp Ile Thr Thr Thr Asn Ser Tyr Glu Lys 370 375 380
- Glu Lys Leu Gln Glu Arg Leu Ala Lys Leu Ser Gly Gly Val Ala Val 385 390 395 400
- Ile Arg Val Gly Gly Ala Ser Glu Val Glu Val Gly Glu Lys Lys Asp 405 410 415
- Arg Tyr Asp Asp Ala Leu Asn Ala Thr Arg Ala Ala Val Glu Glu Gly 420 425 430
- Ile Leu Pro Gly Gly Gly Thr Ala Leu Val Lys Ala Ser Arg Val Leu 435 440 445
- Asp Glu Val Val Val Asp Asn Phe Asp Gln Lys Leu Gly Val Asp Ile 450 455 460
- Ile Arg Lys Ala Ile Thr Arg Pro Ala Lys Gln Ile Ile Glu Asn Ala 465 470 475 480
- Gly Glu Glu Gly Ser Val Ile Ile Gly Lys Leu Ile Asp Glu Tyr Gly
 485 490 495
- Asp Asp Phe Ala Lys Gly Tyr Asp Ala Ser Lys Ser Glu Tyr Thr Asp 500 505 510
- Met Leu Ala Thr Gly Ile Ile Asp Pro Phe Lys Val Val Arg Ser Gly 515 520 525
- Leu Val Asp Ala Ser Gly Val Ala Ser Leu Leu Ala Thr Thr Glu Val 530 540
- Ala Ile Val Asp Ala Pro Glu Pro Pro Ala Ala Ala Gly Ala Gly 545 550 560

Met Pro Gly Gly Met Pro Gly Met Pro Gly Met Met 565 570

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 577 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Ile Ser Thr Leu Arg Gly Lys Ile Phe Asn Asn Gly Ser Asn Arg 1 5 10 15

Asn Lys Cys Val Ser Ile Leu Ser Asn Ile Gln Lys Arg Asn Ile Ser 20 25 30

Lys Asp Ile Arg Phe Gly Ser Asp Ala Arg Thr Ala Met Leu Thr Gly 35 40 45

Cys Asn Lys Leu Ala Asp Ala Val Ser Val Thr Leu Gly Pro Lys Gly 50 55 60

Arg Asn Val Ile Ile Glu Gln Ser Phe Gly Ser Pro Lys Ile Thr Lys 65 70 75 80

Asp Gly Val Thr Val Ala Lys Ser Ile Glu Phe Asn Asn Lys Leu Ala 85 90 95

Asn Leu Gly Ala Gln Met Val Lys Gln Val Ala Ala Asn Thr Asn Gly
100 105 110

Lys Ala Gly Asp Gly Thr Thr Thr Ala Thr Ile Leu Ala Arg Ser Ile 115 120 125

Phe Gln Gln Gly Cys Lys Ala Val Asp Ser Gly Met Asn Pro Met Asp 130 135 140

Leu Leu Arg Gly Ile Asn Lys Gly Val Glu Lys Val Leu Glu Tyr Leu 145 150 155 160

Asn Ser Ile Lys Lys Asp Val Thr Thr Thr Glu Glu Ile Phe Asn Val 165 170 175

Ala Ser Ile Ser Asn Gly Asp Lys Asn Ile Gly Gln Leu Ile Ala Asp 180 185 190

Thr Met Lys Lys Val Gly Lys Glu Gly Thr Ile Thr Val Thr Glu Gly
195 200 205

Lys Thr Leu Gln His Glu Leu Glu Ile Val Glu Gly Ile Lys Phe Asp 210 215 220

Arg 225	Gly	Tyr	Ile	Ser	Pro 230	Tyr	Phe	Ile	Asn	Asn 235	Ser	Gln	Lys	Val	Glu 240		
Leu	Asp	Lys	Pro	Tyr 245	Ile	Leu	Ile	His	Glu 250	Lys	Lys	Ile	Ser	Thr 255	Val		
Lys	Ser	Leu	Leu 260	Pro	Val	Leu	Glu	His 265	Val	Leu	Gln	Asn	Gln 270	Ser	Ser		
Leu	Leu	Val 275	Ile	Ala	Glu	Asp	Val 280	Asp	Ser	Asp	Ala	Leu 285	Ala	Thr	Leu		
Ile	Val 290	Asn	Lys	Leu	Arg	Leu 295	Gly	Leu	Lys	Ile	Cys 300	Ala	Val	Lys	Ala		
Pro 305	Gly	Phe	Gly	Glu	His 310	Arg	Lys	Ala	Leu	Ile 315	His	Asp	Ile	Ala	Val 320		
Met	Thr	Gly	Ala	Lys 325	Val	Ile	Thr	Glu	Glu 330	Thr	Gly	Leu	Lys	Leu 335	Asp		
Asp	Pro	Gln	Val 340	Val	Ser	Tyr	Leu	Gly 345	Lys	Ala	Lys	Ser	Ile 350	Asn	Val		
Thr	Lys	Asp 355	Ser	Thr	Leu	Ile	Met 360	Glu	Gly	Glu	Gly	Lys 365	Lys	Glu	Glu		
Ile	Asn 370	Glu	Arg	Cys	Glu	Ser 375	Ile	Arg	Asn	Ala	Ile 380	Lys	Met	Asn	Thr		
Ser 385	Asp	Tyr	Glu	Lys	Glu 390	Lys	Leu	Gln	Glu	Arg 395	Leu	Ala	Lys	Ile	Thr 400		
Gly	Gly	Val	Ala	Leu 405	Ile	Lys	Val	Gly	Gly 410	Ile	Ser	Glu	Val	Glu 415	Val		
Asn	Glu	Ile	Lys 420	Asp	Arg	Ile	Gln	Asp 425	Ala	Leu	Cys	Ala	Thr 430	Lys	Ala		
Ala	Val	Glu 435	Glu	Gly	Ile	Val	Pro 440	Gly	Gly	Gly	Ser	Ala 445	Leu	Leu	Phe		
Ala	Ser 450	Lys	Glu	Leu	Asp	Ser 455	Val	Gln	Thr	Asp	Asn 460	Tyr	Asp	Gln	Arg		
Val 465	Gly	Val	Asn	Ile	Ile 470	Lys	Asp	Ala	Cys	Lys 475	Ala	Pro	Ile	Lys	Gln 480		
Ile	Ala	Glu	Asn	Ala 485	Gly	His	Glu	Gly	Ser 490	Val	Val	Ala	Gly	Asn 495	Ile		
Leu	Lys	Asp	Lys 500	Asn	Ser	Asn	Ile	Gly 505	Phe	Asn	Ala	Gln	Glu 510	Gly	Lys		
Tyr	Val	Asp 515	Met	Ile	Glu	Ser	Gly 520	Ile	Ile	Asp	Pro	Thr 525	Lys	Val	Val		

Lys Thr Ala Ile Ser Asp Ala Ala Ser Ile Ala Ser Leu Met Thr Thr 530 535 540

Thr Glu Val Ala Ile Val Asp Phe Lys Asp Ser Lys Asn Glu Glu Ser 545 550 555 560

Ser Gln His Met Asn Ser Val Asn Ser Met Gly Asp Met Gly Met 565 570 575

Tyr

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 550 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Thr Asn Val Val Val Ser Gly Glu Gln Leu Gln Gln Ala Phe Arg

1 10 15

Glu Val Ala Ala Val Ile Asp Ser Thr Val Ala Val Thr Ala Gly Pro 20 25 30

Arg Gly Lys Thr Val Gly Ile Asn Lys Pro Tyr Gly Ala Pro Glu Ile 35 40 45

Thr Lys Asp Gly Tyr Lys Val Met Lys Gly Ile Lys Pro Glu Lys Pro 50 60

Leu Asn Ala Ala Ile Thr Ser Ile Phe Ala Gln Ser Cys Ser Gln Cys 65 70 75 80

Asn Asp Lys Val Gly Asp Gly Thr Thr Thr Cys Ser Ile Leu Thr Ser 85 90 95

Gly Met Ile Val Glu Ala Ser Lys Ser Ile Ala Ala Gly Asn Asp Arg 100 105 110

Ile Ser Ile Lys Asn Gly Met Gln Lys Ala Lys Asp Val Val Leu Lys 115 120 125

Glu Val Ala Ser Met Ala Arg Thr Ile Ser Leu Glu Lys Ile Asp Glu 130 135 140

Val Ala Gln Val Ala Ile Ile Ser Ala Asn Gly Asp Arg Ser Ile Gly 145 150 155 160

Ser Asn Ile Ala Asp Ala Val Lys Lys Val Gly Lys Glu Gly Val Ile 165 170 175

- Thr Val Glu Glu Ser Lys Gly Ser Lys Glu Leu Glu Val Glu Leu Thr 180 185 190
- Thr Gly Met Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Ile Thr 195 200 205
- Asn Asn Glu Lys Met Ile Val Glu Leu Asp Asp Pro Tyr Leu Leu Ile 210 215 220
- Thr Glu Lys Lys Leu Asn Ile Ile Gln Pro Leu Leu Ser Ile Leu Glu 225 230 235 240
- Ala Val Val Lys Ser Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Ile 245 250 255
- Glu Gly Glu Ala Leu Ser Thr Leu Val Ile Asn Lys Leu Arg Gly Gly 260 265 270
- Leu Lys Val Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys 275 280 285
- Glu Met Leu Glu Asp Ile Ala Ala Leu Thr Asn Ala Lys Tyr Val Ile 290 295 300
- Lys Asp Glu Leu Gly Ile Lys Met Glu Asp Leu Thr Leu Glu Asp Leu 305 310 315 320
- Gly Ile Ala Lys Asn Val Lys Ile Thr Lys Asp Asn Thr Thr Ile Val 325 330 335
- Ser Glu Asn Arg Val Thr Asp Arg Val Lys Ala Arg Ile Glu Gln Ile 340 345 350
- Lys Ser Gln Ile Glu Ser Ser Thr Ser Asp Tyr Asp Lys Glu Lys Leu 355 360 365
- Arg Glu Arg Leu Ala Lys Leu Ser Gly Gly Val Ala Val Leu Lys Val 370 380
- Gly Gly Ala Thr Glu Leu Glu Val Lys Glu Arg Arg Asp Arg Val Glu 385 390 395 400
- Asp Gln Leu His Ala Thr Arg Ala Ala Ile Glu Glu Gly Ile Val Pro 405 410 415
- Gly Gly Val Ala Leu Leu Tyr Ala Ser Ser Ala Leu Asp Lys Leu 420 425 430
- Lys Gly Ala Asp Asp Glu Glu Gln Ile Gly Ile Asn Ile Ile Lys Lys 435 440 445
- Val Leu Ser Val Pro Ile Lys Arg Leu Val Lys Asn Ala Gly Leu Glu 450 455 460
- Ser Ala Val Ile Ile Asp Tyr Leu Ile Lys Gln Asn Asn Lys Glu Leu 465 470 475 480

Ile Tyr Asn Val Glu Ala Met Ser Tyr Ala Asn Ala Phe Ala Ala Gly
485 490 495

Val Ile Asp Pro Ala Lys Val Val Arg Ile Ala Phe Glu Thr Ala Ile 500 505 510

Ser Val Ala Ser Val Leu Ile Thr Thr Glu Ser Met Ile Val Asp Ile 515 520 525

Pro Asn Lys Asp Glu Asn Ala Ser Ser Pro Met Gly Ala Gly Gly Met 530 535 540

Gly Arg Met Asn Asp Phe 545 550

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 568 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Leu Arg Leu Ala Arg Lys Gly Leu Gln Thr Ala Val Val Arg Ser 1 5 10 15

Tyr Ala Lys Asp Val Lys Phe Gly Ala Glu Gly Arg Gln Ala Met Leu 20 25 30

Val Gly Val Asn Leu Leu Ala Asp Ala Val Ser Val Thr Met Gly Pro 35 40 45

Lys Gly Arg Asn Val Ile Ile Glu Gln Ser Trp Gly Ser Pro Lys Ile 50 55 60

Thr Lys Asp Gly Val Thr Val Ala Lys Ser Ile Asp Leu Lys Asp Lys 65 70 75 80

Tyr Gln Asn Leu Gly Ala Lys Leu Ile Gln Asp Val Ala Asn Lys Ala 85 90 95

Asn Glu Glu Ala Gly Asp Gly Thr Thr Cys Ala Thr Val Leu Thr Arg 100 105 110

Ala Ile Ala Lys Glu Gly Phe Glu Arg His Ser Ser Arg Gly Asn Ala 115 120 125

Val Glu Ile Arg Arg Gly Val Met Asn Ala Val Glu Val Val Val Ala 130 135 140

Glu Leu Lys Lys Ile Ser Lys Lys Val Thr Thr Pro Glu Glu Ile Ala 145 150 155 160

170 Ile Ser Asp Ala Met Lys Lys Val Gly Thr Thr Gly Val Ile Thr Val 180 185 Lys Asp Gly Lys Thr Leu Asn Asp Gln Leu Glu Leu Ile Glu Gly Met Lys Phe Asp Arg Gly Tyr Ile Ser Pro Tyr Phe Ile Thr Ser Ala Lys Gly Ala Lys Val Glu Tyr Glu Lys Ala Leu Val Leu Leu Ser Glu Lys 230 235 Lys Ile Ser Gln Val Gln Asp Ile Val Pro Ala Leu Glu Leu Ala Asn 245 250 Lys Leu Arg Arg Pro Leu Val Ile Ile Ala Glu Asp Val Asp Gly Glu Ala Leu Thr Thr Leu Val Leu Asn Arg Leu Lys Val Gly Leu Gln Val 280 Val Ala Ile Lys Ala Pro Gly Phe Gly Asp Asn Arg Lys Asn Ala Leu 295 300 Lys Asp Met Gly Ile Ala Thr Gly Ala Ser Ile Phe Gly Asp Glu Thr 305 310 315 Leu Asp Leu Arg Leu Glu Asp Ile Thr Ala Asn Asp Leu Gly Glu Val 330 Asp Glu Val Thr Ile Thr Lys Asp Asp Thr Leu Leu Arg Gly Arg 340 345 Gly Asp Gln Thr Glu Ile Glu Lys Arg Ile Glu Glu Ile Thr Asp Glu 360 Ile Glu Arg Ser Thr Ser Asp Tyr Glu Lys Glu Lys Leu Asn Glu Arg 370 375 380

Gln Val Ala Thr Ile Ser Ala Asn Gly Asp Thr Val Val Gly Asn Leu

Ser Glu Val Glu Val Gly Glu Lys Lys Asp Arg Val Thr Asp Ala Leu 405 410 410 Gly Gly Gly Gly Gly 420 425 Gly Asp Arg Val Thr Asp Ala Leu 415

Leu Ala Lys Leu Ser Lys Gly Val Ala Val Leu Lys Ile Gly Gly Gly

- Val Ala Leu Leu Arg Ser Leu Thr Ala Leu Lys Asn Tyr Lys Ala Ala 435 440 445
- Asn Glu Asp Gln Gln Ile Gly Val Asn Ile Val Lys Lys Ala Leu Thr 450 455 460

Gln Pro Ile Ala Thr Ile Val Lys Asn Ala Gly Leu Glu Pro Ser Ser 465 470 475 480

Ile Ile Asp Glu Val Thr Gly Asn Ser Asn Thr Ser Tyr Gly Tyr Asp 485 490 495

Ala Leu Asn Gly Lys Phe Val Asp Met Phe Glu Ala Gly Ile Ile Asp 500 505 510

Pro Thr Lys Val Val Arg Thr Ala Leu Gln Asp Ala Ser Gly Val Ala 515 520 525

Ser Leu Leu Ala Thr Thr Glu Cys Val Val Thr Glu Ile Pro Lys Glu 530 535 540

Glu Ala Val Gly Gly Pro Ala Gly Gly Met Gly Gly Met Gly Gly Met 545 550 555 560

Gly Gly Met Gly Gly Met Gly Phe 565

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 576 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Phe Arg Leu Pro Val Ser Leu Ala Arg Ser Ser Ile Ser Arg Gln 1 10 15

Leu Ala Met Arg Gly Tyr Ala Lys Asp Val Arg Phe Gly Pro Glu Val 20 25 30

Arg Ala Met Met Leu Gln Gly Val Asp Val Leu Ala Asp Ala Val Ala 35 40 45

Val Thr Met Gly Pro Lys Gly Arg Asn Val Ile Ile Glu Gln Ser Val 50 55 60

Gly Leu Ala Lys Ile Thr Lys Asp Gly Val Thr Val Ala Lys Ser Ile 65 70 75 80

Glu Leu Lys Asp Lys Phe Gln Asn Ile Gly Ala Lys Leu Val Gln Asp 85 90 95

Leu Ala Asn Asn Thr Asn Glu Glu Ala Gly Asp Gly Thr Thr Thr Ala
100 105 110

Thr Phe Leu Ala Arg Ala Ile Ala Lys Glu Gly Phe Glu Lys Ile Ser 115 120 125

Lys	Gly 130	Gly	Asn	Pro	Val	Glu 135	Ile	Arg	Arg	Gly	Val 140	Met	Leu	Ala	Val
Glu 145	Thr	Val	Lys	Asp	Asn 150	Leu	Lys	Thr	Met	Ser 155	Arg	Pro	Val	Ser	Thr 160
Pro	Glu	Glu	Ile	Ala 165	Gln	Val	Ala	Thr	Ile 170	Ser	Ala	Asn	Gly	Asp 175	Arg
Glu	Ile	Gly	Asn 180	Gly	Lys	Val	Ser	Val 185	Ser	Glu	Ala	Met	Lys 190	Lys	Val
Gly	Arg	Asp 195	Gly	Val	Ile	Thr	Val 200	Lys	Asp	Gly	Lys	Thr 205	Leu	Thr	Asp
Glu	Leu 210	Glu	Val	Ile	Glu	Gly 215	Thr	Met	Arg	Phe	Asp 220	Arg	Gly	Tyr	Ile
Ser 225	Pro	Tyr	Phe	Ile	Asn 230	Ser	Ser	Lys	Gly	Ala 235	Lys	Val	Glu	Phe	Gln 240
Asp	Ala	Leu	Leu	Leu 245	Leu	Ser	Glu	Lys	Lys 250	Ile	Ser	Ser	Val	Ala 255	Glu
His	His	Ser	Pro 260	Leu	Trp	Arg	Leu	Ala 265	Ser	Arg	Arg	Thr	Arg 270	Lys	Pro
		275				Asp	280	_	_			285			
	290					Ile 295					300				
305				_	310	Arg	_			315		_			320
	-	_		325		Gly		_	330				-	335	
			340			Leu		345					350		
		355				Leu	360					365			*
	370					Ile 375					380				
385					390	Leu				395					400
				405		Gly			410					415	
Lys	Lys	Asp	Arg 420	Val	His	Asp	Ala	Leu 425	Asn _.	Ala	Thr	Arg	Ala 430	Ala	Val

- Glu Glu Gly Ile Val Pro Gly Gly Gly Arg Pro Leu Leu Arg Cys Ile 435 440 445
- Glu Lys Leu Glu Gly Val Glu Thr Thr Asn Glu Asp Gln Lys Leu Gly 450 455 460
- Val Glu Ile Val Arg Arg Ala Leu Arg Met Pro Cys Met Thr Ile Ala 465 470 475 480
- Lys Asn Ala Gly Val Asp Gly Ala Met Val Val Ala Lys Val Glu Asn 485 490 495
- Gln Ala Gly Asp Tyr Gly Tyr Asp Ala Lys Gly Glu Tyr Gly Asn Leu 500 505 510
- Ile Glu Lys Gly Ile Ile Asp Pro Thr Lys Val Val Arg Thr Ala Ile 515 520 525
- Thr Asp Ala Ser Gly Val Ala Ser Leu Leu Thr Thr Ala Glu Ala Val 530 540
- Val Thr Glu Ile Pro Lys Glu Asp Gly Ala Pro Ala Met Pro Gly Met 545 550 550 560
- Gly Gly Met Gly Gly Met Gly Gly Met Gly Gly Met Met 565 570 575

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 573 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

- Met Leu Arg Leu Pro Thr Val Phe Arg Gln Met Arg Pro Val Ser Arg 1 5 10 15
- Val Leu Ala Pro His Leu Thr Arg Ala Tyr Ala Lys Asp Val Lys Phe 20 25 30
- Gly Ala Asp Ala Arg Ala Leu Met Leu Gln Gly Val Asp Leu Leu Ala 35 40 45
- Asp Ala Val Ala Val Thr Met Gly Pro Lys Gly Arg Thr Val Ile Ile 50 60
- Glu Gln Gly Trp Gly Ser Pro Lys Val Thr Lys Asp Gly Val Thr Val 65 70 75 80
- Ala Lys Ser Ile Asp Leu Lys Asp Lys Tyr Lys Asn Ile Gly Ala Lys

Leu Val Gln Asp Val Ala Asn Asn Thr Asn Glu Glu Ala Gly Asp Gly Thr Thr Ala Thr Val Leu Ala Arg Ser Ile Ala Lys Glu Gly Phe Glu Lys Ile Ser Lys Gly Ala Asn Pro Val Glu Ile Arg Arg Gly Val Met Leu Ala Val Asp Ala Val Ile Ala Glu Leu Lys Lys Gln Ser Lys Pro Val Thr Thr Pro Glu Glu Ile Ala Gln Val Ala Thr Ile Ser Ala Asn Gly Asp Lys Glu Ile Gly Asn Ile Ile Ser Asp Ala Met Lys Lys Val Gly Arg Lys Gly Val Ile Thr Val Lys Asp Gly Lys Thr Leu Asn Asp Glu Leu Glu Ile Ile Glu Gly Met Lys Phe Asp Arg Gly Tyr Ile Ser Pro Tyr Phe Ile Asn Thr Ser Lys Gly Gln Lys Cys Glu Phe Gln Asp Ala Tyr Val Leu Leu Ser Glu Lys Lys Ile Ser Ser Ile Gln Ser Ile Val Pro Ala Leu Glu Ile Ala Asn Ala His Arg Lys Pro Leu Val Ile Ile Ala Glu Asp Val Asp Gly Glu Ala Leu Ser Thr Leu Val Leu Asn Arg Leu Lys Val Gly Leu Gln Val Val Ala Val Lys Ala Pro Gly Phe Gly Asp Asn Arg Lys Asn Gln Leu Lys Asp Met Ala Ile Ala Thr Gly Gly Ala Val Phe Gly Glu Glu Gly Leu Thr Leu Asn Leu Glu Asp Val Gln Pro His Asp Leu Gly Lys Val Gly Glu Val Ile Val Thr Lys Asp Asp Ala Met Leu Lys Gly Lys Gly Asp Lys Ala Gln Ile Glu Lys Arg Ile Gln Glu Ile Ile Glu Gln Leu Asp Val Thr Thr Ser Glu Tyr Glu Lys Glu Lys Leu Asn Glu Arg Leu Ala Lys Leu Ser Asp Gly

- Val Ala Val Leu Lys Val Gly Gly Thr Ser Asp Val Glu Val Asn Glu 405 410 415
- Lys Lys Asp Arg Val Thr Asp Ala Leu Asn Ala Thr Arg Ala Ala Val 420 425 430
- Glu Glu Gly Ile Val Leu Gly Gly Gly Cys Ala Leu Leu Arg Cys Ile 435 440 445
- Pro Ala Leu Asp Ser Leu Thr Pro Ala Asn Glu Asp Gln Lys Ile Gly 450 455 460
- Ile Glu Ile Ile Lys Arg Thr Leu Lys Ile Pro Ala Met Thr Ile Ala 465 470 475 480
- Lys Asn Ala Gly Val Glu Gly Ser Leu Ile Val Glu Lys Ile Met Gln 485 490 495
- Ser Ser Ser Glu Val Gly Tyr Asp Ala Met Ala Gly Asp Phe Val Asn 500 505 510
- Met Val Glu Lys Gly Ile Ile Asp Pro Thr Lys Val Val Arg Thr Ala 515 520 525
- Leu Leu Asp Ala Ala Gly Val Ala Ser Leu Leu Thr Thr Ala Glu Val 530 535 540
- Val Val Thr Glu Ile Pro Lys Glu Glu Lys Asp Pro Gly Met Gly Ala 545 550 555 560
- Met Gly Gly Met Gly Gly Met Gly Gly Met Phe 565 570

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 577 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

- Met Tyr Arg Phe Ala Ser Asn Leu Ala Ser Lys Ala Arg Ile Ala Gln 1 5 10 15
- Asn Ala Arg Gln Val Ser Ser Arg Met Ser Trp Ser Arg Asn Tyr Ala 20 25 30
- Ala Lys Glu Ile Lys Phe Gly Val Glu Ala Arg Ala Leu Met Leu Lys 35 40 45
- Gly Val Glu Asp Leu Ala Asp Ala Val Lys Val Thr Met Gly Pro Lys

Gly Arg Asn Val Val Ile Glu Gln Ser Trp Gly Ala Pro Lys Val Thr Lys Asp Gly Val Thr Val Ala Lys Ser Ile Glu Phe Lys Asp Lys Ile Lys Asn Val Gly Ala Ser Leu Val Lys Gln Val Ala Asn Ala Thr Asn Asp Val Ala Gly Asp Gly Thr Thr Cys Ala Thr Val Leu Thr Arg Ala Ile Phe Ala Glu Gly Cys Lys Ser Val Ala Ala Gly Met Asn Ala Met Asp Leu Arg Arg Gly Ile Ser Met Ala Val Asp Ala Val Val Thr Asn Leu Lys Ser Lys Ala Arg Met Ile Ser Thr Ser Glu Glu Ile Ala Gln Val Gly Thr Ile Ser Ala Asn Gly Glu Arg Glu Ile Gly Glu Leu Ile Ala Lys Ala Met Glu Lys Val Gly Lys Glu Gly Val Ile Thr Ile Gln Asp Gly Lys Thr Leu Phe Asn Glu Leu Glu Val Val Glu Gly Met Lys Leu Asp Arg Gly Tyr Thr Ser Pro Tyr Phe Ile Thr Asn Gln Lys Thr Gln Lys Cys Glu Leu Asp Asp Pro Leu Ile Leu Ile His Glu Lys Lys Ile Ser Ser Ile Asn Ser Ile Val Lys Val Leu Glu Leu Ala Leu Lys Arg Gln Arg Pro Leu Leu Ile Val Ser Glu Asp Val Glu Ser Asp Ala Leu Ala Thr Leu Ile Leu Asn Lys Leu Arg Ala Gly Ile Lys Val Cys Ala Ile Lys Ala Pro Gly Phe Gly Glu Asn Arg Lys Ala Asn Leu Gln Asp Leu Ala Ala Leu Thr Gly Gly Glu Val Ile Thr Asp Glu Leu Gly Met Asn Leu Glu Lys Val Asp Leu Ser Met Leu Gly Thr Cys Lys Val Thr Val Ser Lys Asp Asp Thr Val Ile Leu Asp Gly Ala Gly Asp

Lys Lys Gly Ile Glu Glu Arg Cys Glu Gln Ile Arg Ser Ala Ile Glu 370 380

Leu Ser Thr Ser Asp Tyr Asp Lys Glu Lys Leu Gln Glu Arg Leu Ala 385 390 395 400

Lys Leu Ser Gly Gly Val Ala Val Leu Lys Ile Gly Gly Ala Ser Glu
405 410 415

Ala Glu Val Gly Glu Lys Lys Asp Arg Val Thr Asp Ala Leu Asn Ala 420 425 430

Thr Lys Ala Ala Val Glu Glu Gly Ile Leu Pro Gly Gly Gly Val Ala 435 440 445

Leu Leu Tyr Ala Ala Arg Glu Leu Glu Lys Leu Pro Thr Ala Asn Phe 450 455 460

Asp Gln Lys Ile Gly Val Gln Ile Ile Gln Asn Ala Leu Lys Thr Pro 465 470 475 480

Val Tyr Thr Ile Ala Ser Asn Ala Gly Val Glu Gly Ala Val Ile Val 485 490 495

Gly Lys Leu Leu Glu Gln Asp Asn Pro Asp Leu Gly Tyr Asp Ala Ala 500 505 510

Lys Gly Glu Tyr Val Asp Met Val Lys Ala Gly Ile Ile Asp Pro Leu 515 520 525

Lys Val Ile Arg Thr Ala Leu Val Asp Ala Ala Ser Val Ser Ser Leu 530 535 540

Leu Thr Thr Glu Ala Val Val Val Asp Leu Pro Lys Asp Glu Ser 545 550 550 555

Glu Ser Gly Ala Ala Gly Gly Gly Met Gly Gly Met Val Val Met Asp
565 570 575

Tyr

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 576 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Tyr Arg Ala Ala Ser Leu Ala Ser Lys Ala Arg Gln Ala Gly

Ser Ser Ser Ala Ala Arg Gln Val Gly Ser Arg Leu Ala Trp Ser Arg Asn Tyr Ala Ala Lys Asp Ile Lys Phe Gly Val Glu Ala Arg Ala Leu Met Leu Arg Gly Val Glu Glu Leu Ala Asp Ala Val Lys Val Thr Met Gly Pro Lys Gly Arg Asn Val Val Ile Glu Gln Ser Phe Gly Ala Pro Lys Val Thr Lys Asp Gly Val Thr Val Ala Lys Ser Ile Glu Phe Lys Asp Arg Val Lys Asn Val Gly Ala Ser Leu Val Lys Gln Val Ala Asn Ala Thr Asn Asp Asn Ala Gly Asp Gly Thr Thr Cys Ala Thr Val Leu Thr Lys Ala Ile Phe Thr Glu Gly Cys Lys Ser Val Ala Ala Gly Met Asn Ala Met Asp Leu Arg Arg Gly Ile Ser Met Ala Val Asp Ala Val Val Thr Asn Leu Lys Gly Met Ala Arg Met Ile Ser Thr Ser Glu Glu Ile Ala Gln Val Gly Thr Ile Ser Ala Asn Gly Glu Arg Glu Ile Gly Glu Leu Ile Ala Lys Ala Met Glu Lys Val Gly Lys Glu Gly Val Ile Thr Ile Ala Asp Gly Asn Thr Leu Tyr Asn Glu Leu Glu Val Val Glu Gly Met Lys Leu Asp Arg Gly Tyr Ile Ser Pro Tyr Phe Ile Thr Asn Ser Lys Ala Gln Lys Cys Glu Pro Glu Asp Pro Leu Ile Leu Ile His Asp Arg Lys Val Thr Asn Met His Ala Val Val Lys Val Leu Glu Met Ala Leu Lys Lys Gln Arg Pro Leu Leu Ile Val Ala Glu Asp Val Glu Ser Glu Ala Leu Gly Thr Leu Ile Ile Asn Lys Leu Arg Ala Gly Ile Lys Val Cys Ala Val Lys Ala Pro Gly Phe Gly Glu Asn Arg Lys Ala

Asn Leu Gln Asp Leu Ala Ile Leu Thr Gly Gly Glu Val Ile Thr Glu 325 330 Glu Leu Gly Met Asn Leu Glu Asn Val Glu Pro His Met Leu Gly Ser 345 Cys Lys Lys Val Thr Val Ser Lys Asp Asp Thr Val Ile Leu Asp Gly 360 Ala Gly Asp Lys Lys Ser Ile Glu Glu Arg Ala Asp Gln Ile Arg Ser 375 Ala Val Glu Asn Ser Thr Ser Asp Tyr Asp Lys Glu Lys Leu Gln Glu 385 390 395 Arg Leu Ala Lys Leu Ser Gly Gly Val Ala Val Leu Lys Ile Gly Gly 410 Ala Ser Glu Ala Glu Val Gly Glu Lys Lys Asp Arg Val Thr Asp Ala Leu Asn Ala Thr Lys Ala Ala Val Glu Glu Gly Ile Val Pro Gly Gly 440 Gly Val Ala Leu Leu Tyr Ala Ser Lys Glu Leu Asp Lys Leu Gln Thr 455 460 Ala Asn Phe Asp Gln Lys Ile Gly Val Gln Ile Ile Gln Asn Ala Leu 470 475 Lys Thr Pro Val His Thr Ile Ala Ser Asn Ala Gly Val Glu Gly Ala 485 490 Val Val Gly Lys Leu Leu Glu Gln Gly Asn Thr Asp Leu Gly Tyr 505 Asp Ala Ala Lys Asp Glu Tyr Val Asp Met Val Lys Ala Gly Ile Ile 520 Asp Pro Leu Lys Val Ile Arg Thr Ala Leu Val Asp Ala Ala Ser Val 530 535 Ser Ser Leu Met Thr Thr Glu Ser Ile Ile Val Glu Ile Pro Lys 545 550 555 Glu Glu Ala Pro Ala Pro Ala Met Gly Gly Met Gly Gly Met Asp Tyr 565 570

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 587 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

- Met Ala Ser Thr Asn Ala Leu Ser Ser Thr Ser Ile Leu Arg Ser Pro 1 5 10 15
- Thr Asn Gln Ala Gln Thr Ser Leu Ser Lys Lys Val Lys Gln His Gly 20 25 30
- Arg Val Asn Phe Arg Gln Lys Pro Asn Arg Phe Val Val Lys Ala Ala 35 40 45
- Ala Lys Asp Ile Ala Phe Asp Gln His Ser Arg Ser Ala Met Gln Ala 50 55 60
- Gly Ile Asp Lys Leu Ala Asp Ala Val Gly Leu Thr Leu Gly Pro Arg 70 75 80
- Gly Arg Asn Val Val Leu Asp Glu Phe Gly Ser Pro Lys Val Val Asn 85 90 95
- Asp Gly Val Thr Ile Ala Arg Ala Ile Glu Leu Pro Asp Pro Met Glu 100 105 110
- Asn Ala Gly Ala Ala Leu Ile Arg Glu Val Ala Ser Lys Thr Asn Asp 115 120 125
- Ser Ala Gly Asp Gly Thr Thr Thr Ala Ser Ile Leu Ala Arg Glu Ile 130 135 140
- Ile Lys Leu Gly Leu Leu Asn Val Thr Ser Gly Ala Asn Pro Val Ser 145 150 155 160
- Ile Lys Lys Gly Ile Asp Lys Thr Val Ala Ala Leu Val Glu Leu
 165 170 175
- Glu Lys Leu Ala Arg Pro Val Lys Gly Gly Asp Asp Ile Lys Ala Val 180 185 190
- Ala Thr Ile Ser Ala Gly Asn Asp Glu Leu Ile Gly Lys Met Ile Ala 195 200 205
- Glu Ala Ile Asp Lys Val Gly Pro Asp Gly Val Leu Ser Ile Glu Ser 210 215 220
- Ser Asn Ser Phe Glu Thr Thr Val Glu Val Glu Glu Gly Met Glu Ile 225 230 235 240
- Asp Arg Gly Tyr Ile Ser Pro Gln Phe Val Thr Asn Pro Glu Lys Ser 245 250 255
- Ile Val Glu Phe Glu Asn Ala Arg Val Leu Ile Thr Asp Gln Lys Ile
 260 265 270
- Ser Ala Ile Lys Asp Ile Ile Pro Leu Leu Glu Lys Thr Thr Gln Leu

275 280 285

Arg	Ala 290	Pro	Leu	Leu	Ile	Ile 295	Ser	Glu	Asp	Ile	Thr 300	Gly	Glu	Ala	Let
Ala 305	Thr	Leu	Val	Val	Asn 310	Lys	Leu	Arg	Gly	Ile 315	Leu	Asn	Val	Ala	Ala 320
Ile	Lys	Ala	Pro	Gly 325	Phe	Gly	Glu	Arg	Arg 330	Lys	Ala	Leu	Leu	Gln 335	Ası
Ile	Ala	Ile	Leu 340	Thr	Gly	Ala	Glu	Phe 345	Gln	Ala	Ser	Asp	Leu 350	Gly	Leu
Leu	Val	Glu 355	Asn	Thr	Thr	Ile	Glu 360	Gln	Leu	Gly	Leu	Ala 365	Arg	Lys	Va:
Thr	Ile 370	Ser	Lys	Asp	Ser	Thr 375	Thr	Ile	Ile	Ala	Asp 380	Ala	Ala	Ser	Lys
Asp 385	Glu	Leu	Gln	Ser	Arg 390	Val	Ala	Gln	Leu	Lys 395	Lys	Glu	Leu	Ser	Glu 400
Thr	Asp	Ser	Ile	Tyr 405	Asp	Ser	Glu	Lys	Leu 410	Ala	Glu	Arg	Ile	Ala 415	Lys
Leu	Ser	Gly	Gly 420	Val	Ala	Val	Ile	Lys 425	Val	Gly	Ala	Ala	Thr 430	Glu	Thi
Glu	Leu	Glu 435	Asp	Arg	Lys	Leu	Arg 440	Ile	Glu	Asp	Ala	Lys 445	Asn	Ala	Thi
Phe	Ala 450	Ala	Ile	Glu	Glu	Gly 455	Ile	Val	Pro	Gly	Gly 460	Gly	Thr	Ala	Let
Val 465	His	Leu	Ser	Gly	Tyr 470	Val	Pro	Ala	Ile	Lys 475	Glu	Lys	Leu	Glu	Asr 480
Ala	Asp	Glu	Arg	Leu 485	Gly	Ala	Asp	Ile	Val 490	Gln	Lys	Ala	Leu	Val 495	Ala
Pro	Ala	Ala	Leu 500	Ile	Ala	Gln	Asn	Ala 505	Gly	Ile	Glu	Gly	Glu 510	Val	Va]
Val	Glu	Lys 515	Ile	Lys	Asn	Gly	Glu 520	Trp	Glu	Val	Gly	Tyr 525	Asn	Ala	Met
Thr	Asp 530	Thr	Tyr	Glu	Asn	Leu 535	Val	Glu	Ser	Gly	Val 540	Ile	Asp	Pro	Ala
Lys 545	Val	Thr	Arg	Cys	Ala 550	Leu	Gln	Asn	Ala	Ala 555	Ser	Val	Ala	Gly	Met 560
Val	Leu	Thr	Thr	Gln 565	Ala	Ile	Val	Val	Glu 570	Lys	Pro	Lys	Pro	Lys 575	Ala
Ala	Val	Ala	Ala 580	Ala	Pro	Gln	Gly	Leu 585	Thr	Ile					

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 545 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Ala Lys Asp Ile Lys Phe Gly Glu Glu Ala Arg Arg Ala Met Leu 1 5 10 15

Arg Gly Val Asn Ala Leu Ala Asp Ala Val Lys Val Thr Leu Gly Pro 20 25 30

Lys Gly Arg Asn Val Val Leu Glu Lys Ser Phe Gly Ala Pro Thr Ile 35 40 45

Thr Lys Asp Gly Val Thr Val Ala Lys Glu Ile Glu Leu Glu Asp Lys 50 55 60

Phe Glu Asn Met Gly Ala Gln Leu Val Lys Glu Val Ala Ser Lys Thr 70 75 80

Asn Asp Val Ala Gly Asp Gly Thr Thr Ala Thr Val Leu Ala Gln 85 90 95

Ala Ile Val Lys Glu Gly Leu Lys Asn Val Ala Ala Gly Ala Asn Pro 100 105 110

Met Asp Leu Arg Arg Gly Ile Asp Lys Ala Val Asp Ala Val Val Glu
115 120 125

Glu Leu Lys Ala Ile Ala Lys Pro Val Glu Thr Lys Glu Glu Ile Ala 130 135 140

Gln Val Ala Thr Ile Ser Ala Asn Gly Asp Glu Glu Ile Gly Glu Leu 145 150 155 160

Ile Ala Glu Ala Met Glu Lys Val Gly Lys Glu Gly Val Ile Thr Val
165 170 175

Glu Glu Gly Lys Thr Leu Glu Thr Glu Leu Glu Val Val Glu Gly Met 180 185 190

Gln Phe Asp Arg Gly Tyr Ile Ser Pro Tyr Phe Ile Thr Asp Ser Glu 195 200 205

Lys Gln Lys Ala Glu Leu Glu Asp Pro Leu Ile Leu Leu Thr Asp Lys 210 215 220

Lys Ile Ser Asn Ile Gln Asp Leu Leu Pro Val Leu Glu Glu Val Ala

225 230 235 240

Gln Ala Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly Glu 245 250 255

Ala Leu Ala Thr Leu Val Val Asn Lys Leu Arg Gly Thr Leu Lys Val
260 265 270

Val Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met Leu 275 280 285

Gln Asp Ile Ala Ile Leu Thr Gly Gly Gln Val Ile Ser Glu Glu Leu 290 295 300

Gly Leu Ser Leu Glu Asp Ala Thr Leu Glu Asp Leu Gly Gln Ala Lys 305 310 315 320

Lys Val Val Val Thr Lys Asp Asp Thr Thr Ile Val Asp Gly Ala Gly 325 330 335

Asp Ala Ala Ile Ala Gly Arg Val Ala Gln Ile Arg Ser Gln Ile Glu 340 345 350

Glu Ser Thr Ser Asp Tyr Asp Lys Glu Lys Leu Gln Glu Arg Leu Ala 355 360 365

Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala Thr Glu 370 380

Val Glu Leu Lys Glu Arg Lys Asp Arg Val Glu Asp Ala Leu Asn Ala 385 390 395 400

Thr Arg Ala Ala Val Glu Glu Gly Ile Val Pro Gly Gly Val Ala 405 410 415

Leu Leu Arg Ala Ala Pro Ala Leu Asp Lys Leu Lys Thr Glu Asn Gly
420 425 430

Asp Glu Ala Thr Gly Val Asn Ile Val Leu Arg Ala Leu Glu Ala Pro 435 440 445

Leu Arg Gln Ile Ala Glu Asn Ala Gly Leu Glu Gly Ser Val Val 450 455 460

Glu Lys Val Lys Asn Ser Glu Ala Gly Gly Tyr Asn Ala Ala Thr Gly 465 470 475 480

Glu Tyr Val Asp Met Ile Ala Ala Gly Ile Ile Asp Pro Thr Lys Val 485 490 495

Thr Arg Ser Ala Leu Gln Asn Ala Ala Ser Val Ala Ser Leu Met Leu 500 505 510

Thr Thr Glu Ala Val Val Asp Lys Pro Glu Lys Glu Ala Ala Pro 515 520 525

Ala Gly Met Pro Gly Met Met Gly Gly Met Gly Gly Met 530 540

Met 545 (2) INFORMATION FOR SEQ ID NO:35: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:	24
(2) INFORMATION FOR SEQ ID NO:36:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:	
TGATCACATC ATNCCNCCCA TNCC	24
(2) INFORMATION FOR SEQ ID NO:37:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:	
CATATGGCAA AAGAAATHAA RTTY	24
(2) INFORMATION FOR SEQ ID NO:38:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

24

TGATCANCCN CCCATNCCNC CCAT	
(2) INFORMATION FOR SEQ ID NO:39: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 16 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:	16
(2) INFORMATION FOR SEQ ID NO:40:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:	
CAGGAAACAG CTATGAC	17
(2) INFORMATION FOR SEQ ID NO:41:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCAACCATCA CGAAAGA

(2) INFO	DRMATION FOR SEQ ID NO:42:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:42:	
ACGGGT	TCACT TTGGTTG	17
(2) INFO	DRMATION FOR SEQ ID NO:43:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:43:	
TTACTA	AATGA CGGGGTA	17
(2) INFO	ORMATION FOR SEQ ID NO:44:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:44:	
TTACCA	AATGA CGGTGTG	17
(2) INFO	DRMATION FOR SEQ ID NO:45:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:	
ACAGGGTCAA TGATTCC	17
(2) INFORMATION FOR SEQ ID NO:46:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:	
ACTGGATCAA TGATACC	17
(2) INFORMATION FOR SEQ ID NO:47:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:	
CCGTACCGTG CTCTGAC	17
(2) INFORMATION FOR SEQ ID NO:48:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:	
ACCACGTTTC AGATCCA	17
(2) INFORMATION FOR SEQ ID NO:49:	

(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:	17
(2) INFORMATION FOR SEQ ID NO:50:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 17 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:	17
(2) INFORMATION FOR SEQ ID NO:51:	Ι,
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:	
GGTATGCAGT TCGACCG	17
(2) INFORMATION FOR SEQ ID NO:52:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:52:	
CCGTGT	TGGT CAAATCC	17
(2) INFO	RMATION FOR SEQ ID NO:53:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:53:	
GGTAAC	TACG GTTACAA	17
(2) INFO	RMATION FOR SEQ ID NO:54:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:54:	
GAGGCC	ACTT CTTTCAC	17
(2) INFO	RMATION FOR SEQ ID NO:55:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:55:	
GGCTTC	CAGC ACTGGCA	17
(2) INFO	RMATION FOR SEQ ID NO:56:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:	
AACTTCAGTC GCAGCAC	17
(2) INFORMATION FOR SEQ ID NO:57:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:	
CCTTGAAAGC CATTGCT	17
(2) INFORMATION FOR SEQ ID NO:58:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:	17
(2) INFORMATION FOR SEQ ID NO:59:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GCTGCAACAG GTGAGTG

(2)	INFORMATION FOR SEQ ID NO:60:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:	
TC	CATGAACAA TGGCTTG	17
(2)	INFORMATION FOR SEQ ID NO:61:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 17 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:	
AC	CGAAGCACA ATGTTAC	17
	INFORMATION FOR SEQ ID NO:62:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:	
ΡĀ	CCACTAAAG ATGGTGT	17
(2)	INFORMATION FOR SEQ ID NO:63:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:	
GCAGTTGCCG CAGCAGT	17
(2) INFORMATION FOR SEQ ID NO:64:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:	
GCTACTCGTG CAGCTGT	17
(2) INFORMATION FOR SEQ ID NO:65:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:	
GTTCTCCGTG CTTTGGA	17
(2) INFORMATION FOR SEQ ID NO:66:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:	
GCACCTGCTG TGACGTT	17
(2) INFORMATION FOR SEQ ID NO:67:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 17 base pairs	

	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:67:	
TC	TTCG	ATGG TGATGAC	17
(2)	INFO	RMATION FOR SEQ ID NO:68:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:68:	
GG	CAAG	AGCT GTTCCGC	17
(2)	INFO	RMATION FOR SEQ ID NO:69:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:69:	
CT	GAGC	CAGT ACGGTTG	17
(2)	INFO	RMATION FOR SEQ ID NO:70:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

GTACTGCAGA	GCGGAAC

(2) INFORMATION FOR SEQ ID NO:71:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:	
ACCGTCTTCA ACGGTGA	17
(2) INFORMATION FOR SEQ ID NO:72:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:	
GTTATCATTG CTGAAGA	17
(2) INFORMATION FOR SEQ ID NO:73:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:	17
ACGGTACCGC CGGTCAG	17
(2) INFORMATION FOR SEQ ID NO:74:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 17 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	

(2) INFORMATION FOR SEQ ID NO:75:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 17 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:	
CGACTGAAGT TGAAATG	17
(2) INFORMATION FOR SEQ ID NO:76:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:	
GCTGTTGAAG AACTGAA	17
(2) INFORMATION FOR SEQ ID NO:77:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(with appropriately and to we are	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:	
GTCTTCAACG GTGATCA	17
(2) INFORMATION FOR SEQ ID NO:78:	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

17

CTGGGCCAGG CTAAACG

	(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
	. xi) SEQUENCE DESCRIPTION: SEQ ID NO:78: TCTACCG CAGCACG	7
(2) I	NFORMATION FOR SEQ ID NO:79:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:	
CTC	TTGATTA TTGCGGA 17	7
(2) I	NFORMATION FOR SEQ ID NO:80:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:	
TTG	TTCAAAA CAAGAGT 17	7
(2) I	NFORMATION FOR SEQ ID NO:81:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:81:	
CGATTAT	TTGT AGAAGGT	17
(2) INFOR	RMATION FOR SEQ ID NO:82:	
(i) ·	SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:82:	
CTTGATA	AACC GCAACAC	17
(2) INFOR	RMATION FOR SEQ ID NO:83:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:83:	
TCCAAAG	GCAC GGAGAAC	17
(2) INFOR	RMATION FOR SEQ ID NO:84:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:84:	
GTGTCAA	AACA TCCAAGA	17
(2) INFOR	RMATION FOR SEQ ID NO:85:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:	
TCTTCGATGG TAATCAC	17
(2) INFORMATION FOR SEQ ID NO:86:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:	
GCAATAATGA GTAATGG 1	L 7
(2) INFORMATION FOR SEQ ID NO:87:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87: ACAGTAATTG TTGAAGG	٠.7
(2) INFORMATION FOR SEQ ID NO:88:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 17 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CAGTGCAATA CGGTTAG

 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:	
AGCTTCCAGA ACCGGCA	17
(2) INFORMATION FOR SEQ ID NO:90:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:	
CTGATCATCG CTGAAGA	17
(2) INFORMATION FOR SEQ ID NO:91:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 16 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

16

ACGGTTATTG TAGAAG

(2) INFORMATION FOR SEQ ID NO:89: